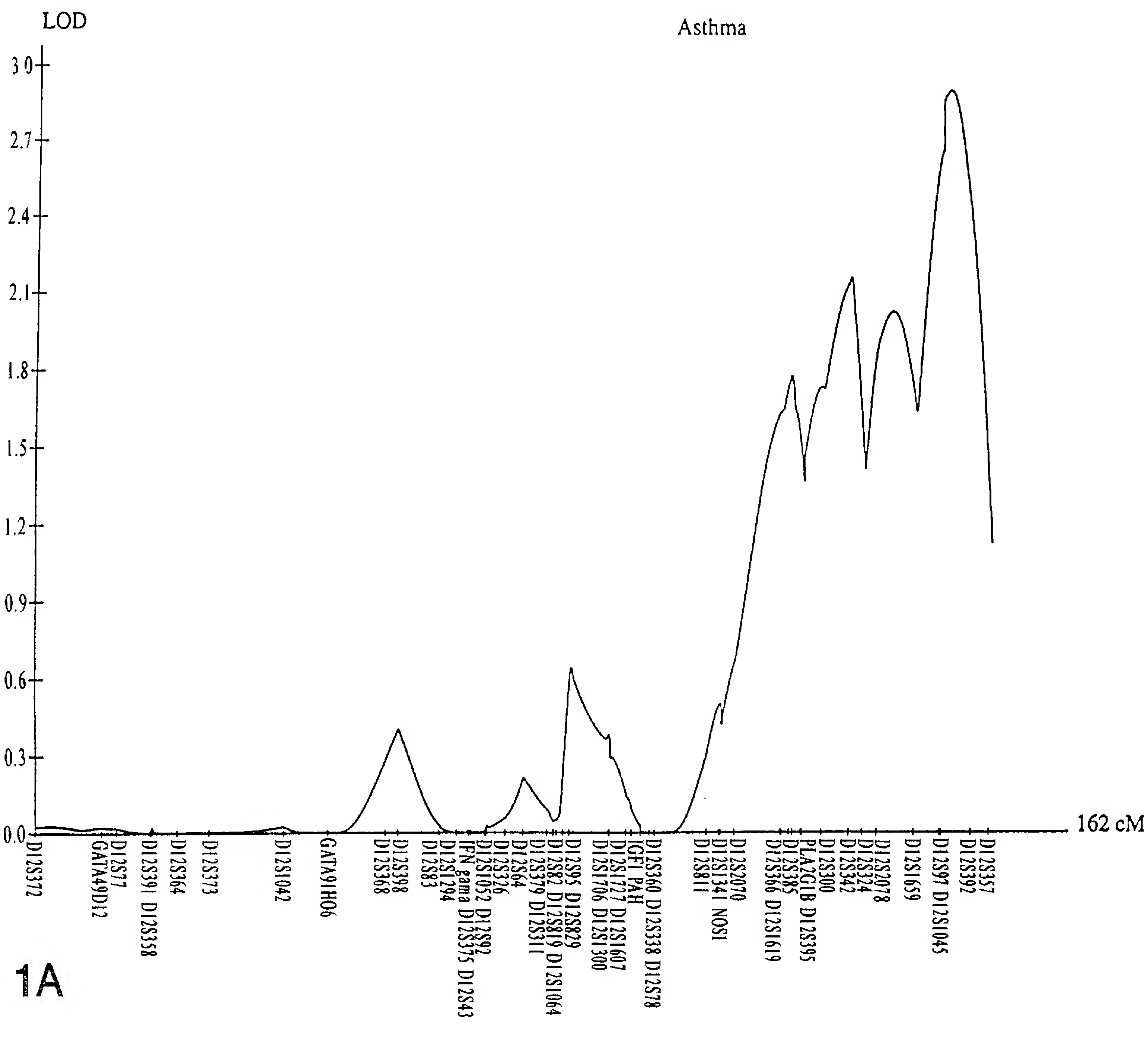

LOD
Asthma
3.0
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0
162 cM
D12S372
GATA49D12
D12S77
D12S391 D12S358
D12S364
D12S373
D12S1042
GATA91H06
D12S368
D12S398
D12S83
D12S1294
IFN gama D12S375 D12S43
D12S1052 D12S92
D12S326
D12S64
D12S379 D12S311
D12S82 D12S819 D12S1064
D12S95 D12S829
D12S1706 D12S1300
D12S1727 D12S1607
IGF1 PAH
D12S360 D12S338 D12S78
D12S811
D12S1341 NOS1
D12S2070
D12S366 D12S1619
D12S385
PLA2G1B D12S395
D12S300
D12S342
D12S324
D12S2078
D12S1659
D12S97 D12S1045
D12S392
D12S357

FIG. 1A

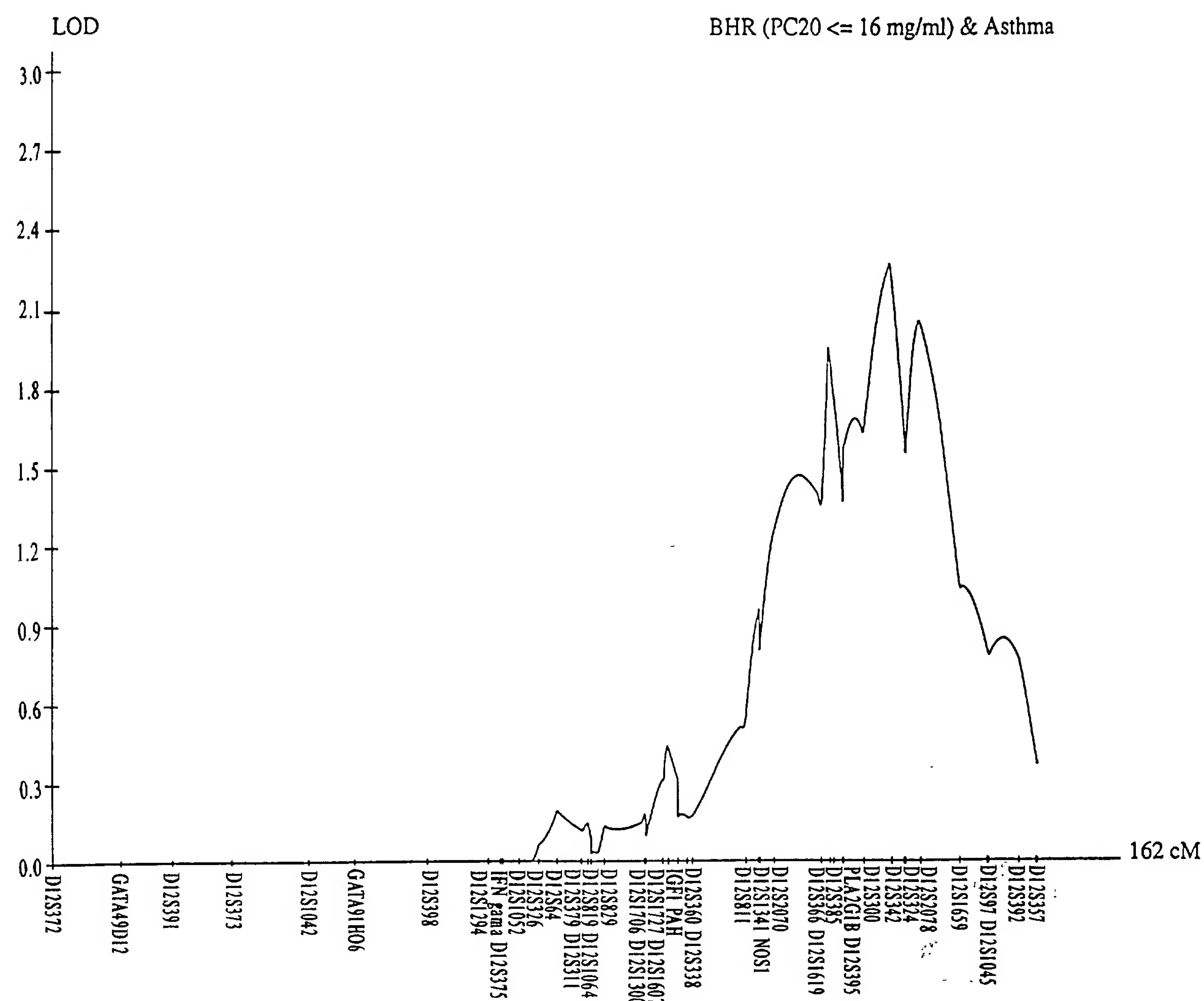
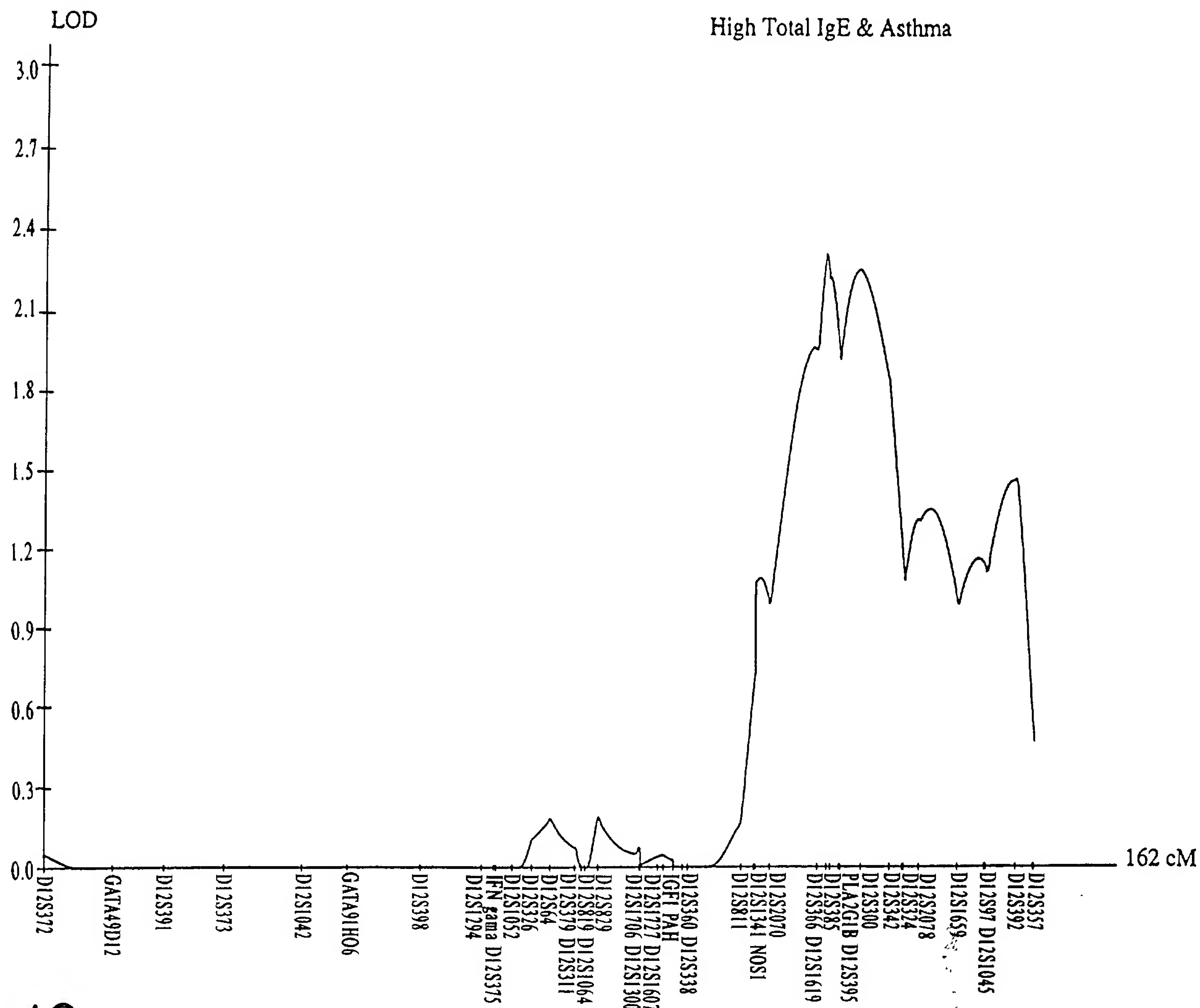
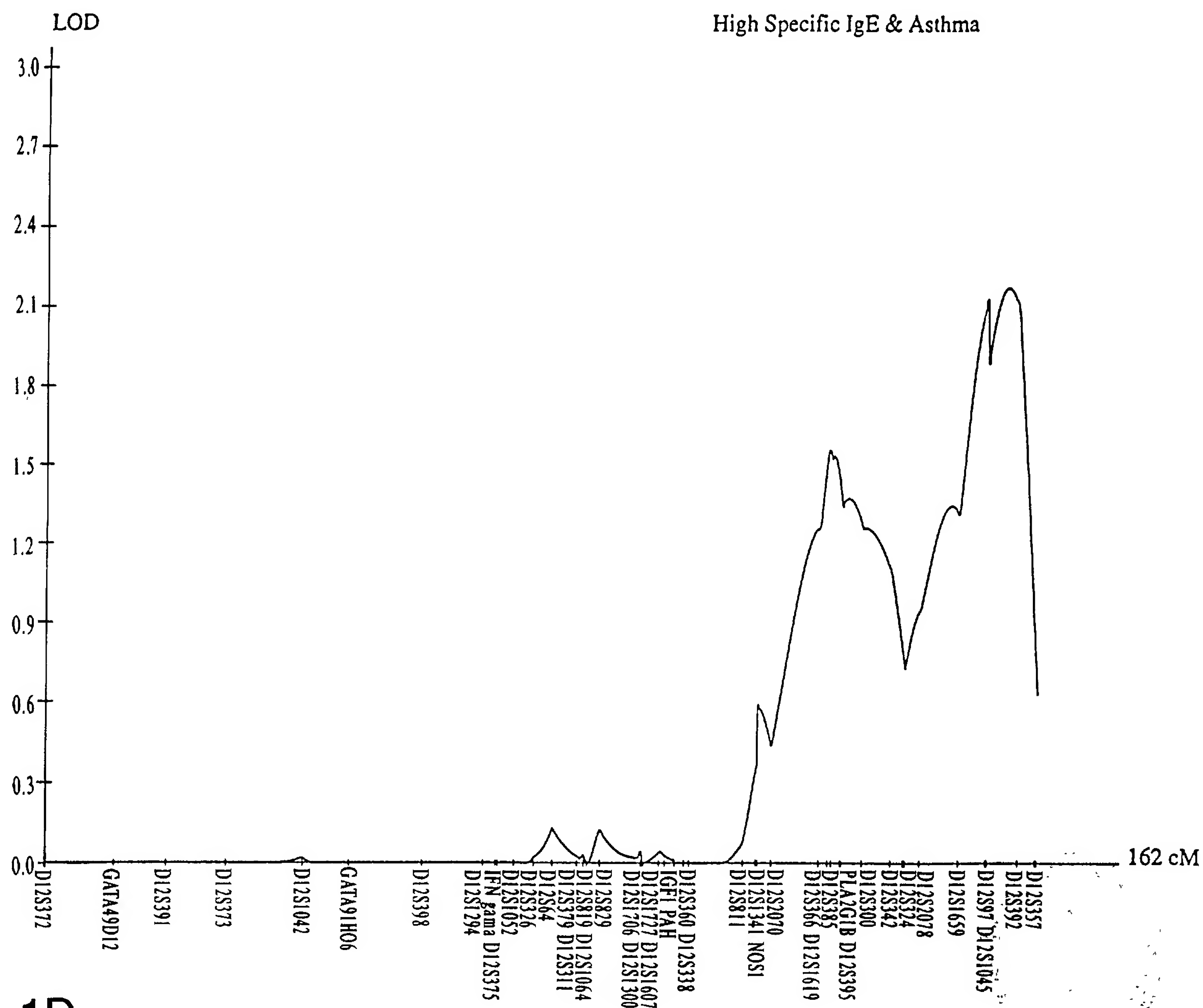

LOD
BHR (PC20 <= 16 mg/ml) & Asthma
3.0
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0
162 cM
D12S372
GATA49D12
D12S391
D12S373
D12S1042
GATA91H06
D12S398
D12S1294
IFN gama D12S375
D12S1052
D12S326
D12S64
D12S379 D12S311
D12S819 D12S1064
D12S829
D12S1706 D12S1300
D12S1727 D12S1607
IGF1 PAH
D12S360 D12S338
D12S811
D12S1341 NOS1
D12S2070
D12S366 D12S1619
D12S385
PLA2G1B D12S395
D12S300
D12S342
D12S324
D12S2078
D12S1659
D12S97 D12S1045
D12S392
D12S357

FIG. 1B



High Total IgE & Asthma
LOD
3.0
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0
162 cM
D12S372
GATA49D12
D12S391
D12S373
D12S1042
GATA91HO6
D12S398
D12S1294
IFN gama D12S375
D12S1052
D12S326
D12S64
D12S379 D12S311
D12S819 D12S1064
D12S829
D12S1706 D12S1300
D12S1727 D12S1607
IGF1 PAH
D12S360 D12S338
D12S811
D12S1341 NOS1
D12S2070
D12S366 D12S1619
D12S385
PLA2G1B D12S395
D12S300
D12S342
D12S324
D12S2078
D12S1659
D12S97 D12S1045
D12S392
D12S357

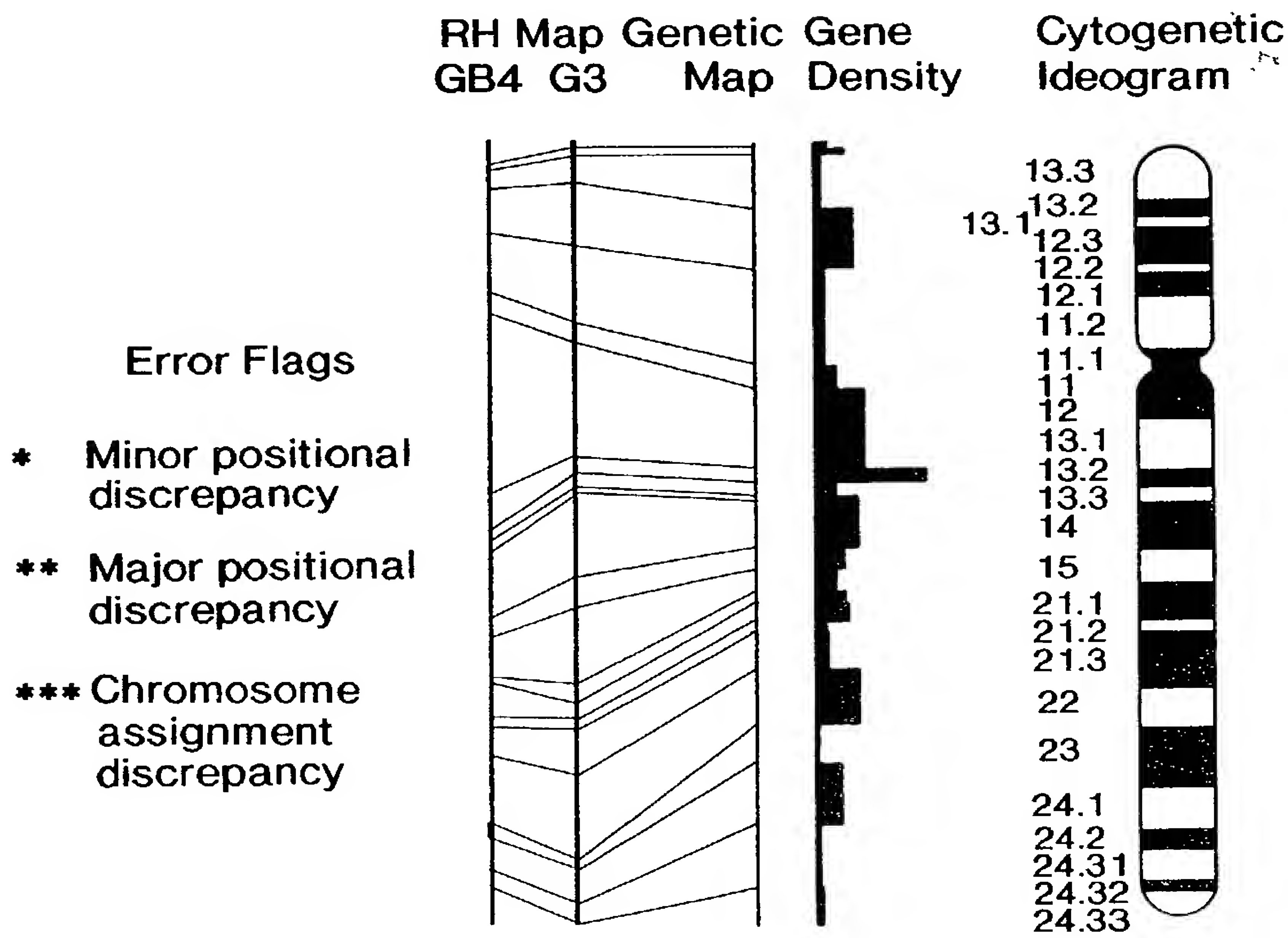
FIG. 1C



LOD
High Specific IgE & Asthma
3.0
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0
162 cM
D12S372
GATA49D12
D12S391
D12S373
D12S1042
GATA91H06
D12S398
D12S1294
IFN gama D12S375
D12S1052
D12S326
D12S64
D12S379 D12S311
D12S819 D12S1064
D12S829
D12S1706 D12S1300
D12S1727 D12S1607
IGF1 PAH
D12S360 D12S338
D12S811
D12S1341 NOS1
D12S2070
D12S366 D12S1619
D12S385
PLA2G1B D12S395
D12S300
D12S342
D12S324
D12S2078
D12S1659
D12S97 D12S1045
D12S392
D12S357

FIG. 1D

Chromosome 12: D12S79-D12S366



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	9 cR_{3000}

FIG. 2A

Next interval up

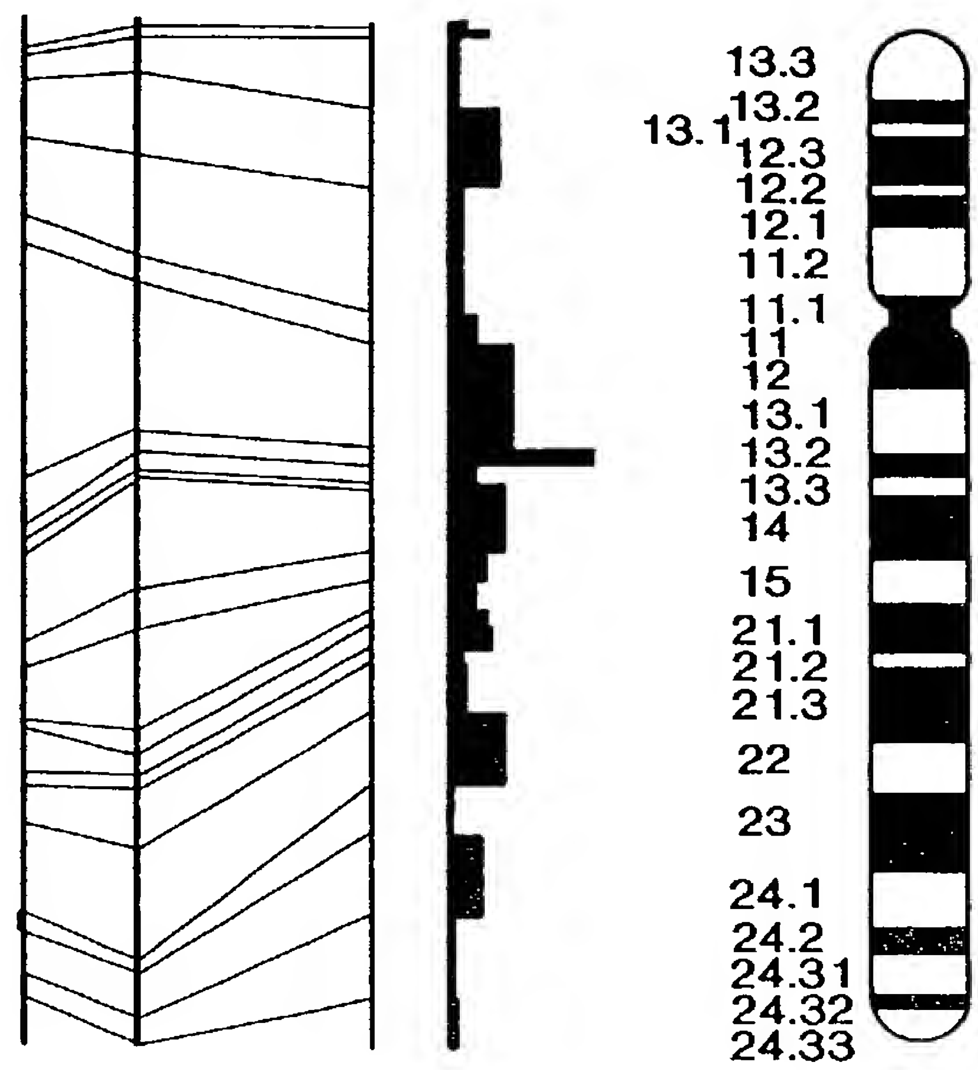
126.1	◆	**451.62**	**F**		**AFM067yc5**	**D12S79**	**Microsatellite anchor marker AFM067yc5**
		454.24	P0.10		A009F32	KIAA0331	KIAA0331 gene product
		455.39	P0.37		sts-N33343		ESTs
		455.39	P1.15		SGC38179		ESTs
		455.70	P0.06		stSG54526		ESTs
		455.81	P1.35		stSG1522		ESTs
		455.86	P2.06		sts-T56610		Homo sapiens mRNA for KIAA0875 protein, p..
		456.02	P2.38		sts-R33659		EST
		456.34	P0.23		sts-D29101		EST
		456.34	P0.04	*	SGC44506		ESTs
		456.86	P2.34		NIB1804		ESTs
		456.86	P>3.00		stSG44263		ESTs, Weakly similar to calcium-binding pr..
		456.86	"		stSG62560		Homo sapiens clone 24852 mRNA sequence
		456.96	P1.66	*	sts-AA001615		ESTs
		456.96	P0.04		sts-T94297		ESTs, Weakly similar to TBX2 gene [H.sapi..
		457.17	P1.31		stSG54365		ESTs
		457.17	P0.13		WI-21497		Homo sapiens mRNA for KIAA0875 protein, p..
		457.17	P0.30		WI-20357		Homo sapiens mRNA for KIAA0875 protein, p..
		457.17	P0.38		SGC31491	NOS1	nitric oxide synthase 1 (neuronal)
		457.17	P0.31		RK903_904	NOS1	nitric oxide synthase 1 (neuronal)
		457.17	P0.18		sts-AA007571		ESTs
		457.17	P1.35		stSG46223		ESTs
		457.17	"		stSG58387		ESTs
	◆	457.27	P>3.00	*	Cda1ce05		Homo sapiens clone 23714 mRNA sequence
		457.27	P0.10	*	sts-W79390	NME2	non-metastatic cells 2, protein (NM23B) exp..
		457.48	P0.20		sts-Z40829		ESTs
		460.94	P0.00	*	A005Q47		ESTs
133.8	◆	460.94	F		AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9

Next interval down

FIG. 2B

Chromosome 12: D12S366-D12S340

RH Map GB4 G3 | Genetic Map | Gene Density | Cytogenetic Ideogram



Error Flags

- * Minor positional discrepancy
- ** Major positional discrepancy
- *** Chromosome assignment discrepancy

The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S366 (133.8 cM)
Bottom of interval:	D12S340 (147.5 cM)
Genetic size of bin:	14 cM
Physical size of bin:	21 cR_{3000}

↑ Next interval up

133.8	◆ 460.94	F		AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
	462.85	P1.00	*	stSG8109		ESTs
	462.85	"		sts-X75252	PBP	prostatic binding protein
	462.95	P1.04		sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2C

	463.77	P0.19		WI-16745		Human clone 37, 5cM region surrounding hepa..
◆	463.77	P0.20		SGC33949	KIAA0262	KIAA0262 gene product
	463.98	P0.02		A008B04		ESTs
	463.98	"		stSG50309		ESTs
	463.98	"		stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
	463.98	P0.04		stSG27318		Human clone 23932 mRNA sequence
	463.98	P0.08		R06295		EST
	463.98	P1.33		sts-W56792		ESTs
	464.08	P2.32		A007E48		ESTs
	464.19	P1.28		A009U43		ESTs
	464.29	P1.33		stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
	464.39	P1.09		sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
	464.39	P1.13		stSG15685	KIAA0262	KIAA0262 gene product
	464.39	"		RP_P0_1	RPLP0	Ribosomal protein large, P0
	464.39	P1.09		stSG29626		ESTs
	464.39	P1.14		stSG31407		Human DNA sequence from BAC 15E1 on chrom..
	464.39	"		A001T32	PXN	paxillin
	464.39	"		A001W18		H.sapiens mRNA for AMP-activated protein ..
	464.39	"		WIAF-40		Human mRNA for KIAA0219 gene, partial cds
	464.39	"		sts-T95105		ESTs
	464.39	"		Cda0id01		ESTs
	464.39	P1.13		stSG31431		ESTs, Moderately similar to (defline not a..
◆	464.39	"	*	WI-13177		Homo sapiens clone 23714 mRNA sequence
	464.39	"		IB1092		Homo sapiens clone 23714 mRNA sequence
	464.39	"		T79466		ESTs
	464.39	P1.18		stSG48379		ESTs
	464.45	P1.05		KIAA0219		Human mRNA for KIAA0219 gene, partial cds
	464.45	"		stSG40392		ESTs
	464.45	"		stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆	464.49	P0.21		A006F12	KIAA0152	KIAA0152 gene product
	464.49	P0.25		sts-AA002185	PXN	paxillin
	464.49	P0.10		stSG48442		ESTs
	464.49	"		sts-T16456		ESTs
	464.49	"		stSG62260		ESTs

FIG. 2D

		464.49	"		NIB1331		ESTs
		464.49	"		WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
		464.49	"		WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
		464.49	"		SGC34758		ESTs
		464.49	"		WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
		464.49	"		IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
		464.49	"		SGC32343		ESTs
		464.79	P0.96		SGC33521		ESTs
		464.79	P0.96	*	X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
		465.20	P0.20		sts-H10302		ESTs
	◆	465.38	P0.85		A007E11	KIAA0262	KIAA0262 gene product
		465.41	P0.81		A007I44	RPLP0	ribosomal protein, large, P0
		465.41	"		stSG22726		EST
		465.41	"		WI-17776		ESTs
		465.41	"		stSG31753		Human mRNA for KIAA0219 gene, partial cds
		465.41	"		stSG31753		Human mRNA for KIAA0219 gene, partial cds
		465.41	P0.77		stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
		465.41	"		A002J47		ESTs, Weakly similar to heat shock protein..
		465.41	P0.80		stSG46660		EST
		465.51	P0.75		stSG41086	PXN	paxillin
		465.51	P0.83		stSG52121		ESTs
		465.91	P0.01		WI-16071		ESTs
		465.91	P0.00		WI-13962		H.sapiens mRNA for AMP-activated protein ..
		466.62	P0.00		sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
		466.71	P0.00		stSG4712		ESTs, Weakly similar to homology with o251..
		466.91	P0.01		WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
		466.91	P0.01		D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
		467.01	P0.01		stSG52567		ESTs
135.1		467.11	F		AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1		467.11	P0.01		AFM299zd5	D12S349	Microsatellite marker AFM299zd5
		467.11	P0.01		AFM123xh2		Unknown
137.5	◆	467.21	P0.02		AFM220zf4	D12S321	Microsatellite marker AFM220zf4
		467.21	P0.02		sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
		467.21	P0.02		stSG8721		EST

FIG. 2E

	467.21	"	stSG44224		ESTs
	467.21	"	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆	467.21	"	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
	467.21	"	stSG47820		ESTs
	467.21	"	Bdac4h06	KIAA0262	KIAA0262 gene product
	467.21	"	stSG15021		ESTs
	467.21	"	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆	467.21	"	H50549	KIAA0262	KIAA0262 gene product
	467.21	P0.03	SGC35167		EST
	467.21	P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
	467.21	P0.02	WIAF-607		Unknown
	467.31	P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
	468.93	P0.85	SGC31344		EST
	469.13	P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
	469.13	P0.14	stSG35104		ESTs
	469.13	"	A006Q41		Unknown
	469.23	P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
	469.33	P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..
	469.33	"	R01708		EST
	469.33	"	stSG54819	HCALB_BR	calbrain
	469.33	"	A001Z45		ESTs, Highly similar to (defline not avail..
	469.33	"	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..
	469.33	"	stSG63173		EST
	469.33	"	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
	469.42	P1.01	WI-16068		EST
	469.44	P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
	469.44	"	stSG62627		EST
	469.44	"	stSG36007		Homo sapiens full length insert cDNA clone..
	469.44	"	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
	469.44	"	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
	469.44	"	stSG62591		ESTs
◆	469.54	P1.03	A006N38	KIAA0152	KIAA0152 gene product
	469.62	P1.03	sts-N34573		ESTs
	469.62	P1.03	sts-N58045		ESTs

FIG. 2F

	469.62	P1.04		WI-13224		EST
	469.83	P1.12		SGC34424		ESTs
	469.93	P1.14		stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
	470.14	P1.17		stSG52516		ESTs, Weakly similar to (defline not avail..
	470.24	P1.32		D0S1735E		ESTs
	470.24	P1.12		WI-6178		ESTs
	470.32	P1.25		sts-U29895		Unknown
	470.32	P1.24		WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
	470.43	P1.29		stSG52094		ESTs
	470.63	P1.38		A004O17		ESTs
◆	470.77	P1.32	**	SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆	470.84	P1.35	**	sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
	470.84	P1.52		WI-13062		Homo sapiens mRNA, expressed in fibroblast..
	471.27	P1.60		sts-R99269		EST
	471.37	P1.70		stSG1991		ESTs
	471.37	"		stSG15859		Homo sapiens full length insert cDNA YQ02..
	471.58	P1.78		stSG29729		ESTs, Weakly similar to (defline not avail..
	471.58	P1.37		WI-16979		ESTs
	471.65	P1.39		WI-17693		EST
	471.80	P1.29		WI-22060		ESTs
	471.90	P>3.00		stSG8210		ESTs, Moderately similar to neuronal threa..
	471.90	"		WI-17956		EST
	471.90	"		WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
	471.90	"		stSG47029		ESTs
	471.90	"		stSG47647		EST
	471.90	"		sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆	471.90	"	**	WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
	471.90	"		NIB962		ESTs
	471.90	"		A009E34		ESTs, Moderately similar to neuronal threa..
	471.90	"		sts-T17477		ESTs
	472.08	P1.49		sts-X89984		H.sapiens mRNA for BCL7A protein
	472.12	P>3.00		SGC34693		EST
	472.12	P>3.00		A009O01		ESTs, Weakly similar to neuronal thread pr..
	472.29	P>3.00		stSG47084		ESTs

FIG. 2G

	472.40	P>3.00		stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
	472.40	P>3.00		AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
	472.61	P>3.00		A002R44		Unknown
	472.61	P>3.00		SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
	472.72	P0.01		sts-H98108		ESTs
	472.97	P>3.00		WI-6239		ESTs
	473.04	P>3.00		sts-H75490		ESTs
◆	473.58	P>3.00	**	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
	474.01	P>3.00		stSG8610		ESTs
	474.01	P>3.00		stSG47080		ESTs
	474.38	P2.18		stSG8686		ESTs, Weakly similar to similar to pre-mRN..
	474.38	P2.25		stSG26358		ESTs, Weakly similar to similar to pre-mRN..
	474.38	"		stSG29931		ESTs
	474.38	"		WI-17926		ESTs
	474.38	"		WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
	474.38	"		1834		EST
	474.38	P2.26		sts-X98258	MPP-9	M phase phosphoprotein 9
	474.38	P2.39		stSG40753		ESTs
	474.64	P>3.00		A004D47		ESTs, Highly similar to There are three pu..
	474.64	P>3.00		sts-N23129	MPP-9	M phase phosphoprotein 9
	474.75	P2.41		sts-AA040696		ESTs
	474.81	P2.37		sts-AA022496		ESTs
	474.81	P2.28		stSG46930	MPP-9	M phase phosphoprotein 9
	474.97	P>3.00		WI-20552	DRP	density-regulated protein
	475.02	P>3.00		SGC30324		ESTs
	475.07	P>3.00		D10923	HM74	putative chemokine receptor; GTP-binding pr..
	475.07	P>3.00		stSG2418	DOC1	Deleted in oral cancer-1
	475.07	"		stSG21321		ESTs
	475.07	"		stSG53515	MPP-9	M phase phosphoprotein 9
	475.07	P>3.00		SGC31687	DOC1	Deleted in oral cancer-1
	475.07	P>3.00		WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
	475.13	P0.79		sts-W93806		ESTs
	475.13	P2.13		stSG48145		ESTs
	475.18	P2.34		A003B12		Homo sapiens full length insert cDNA clone..

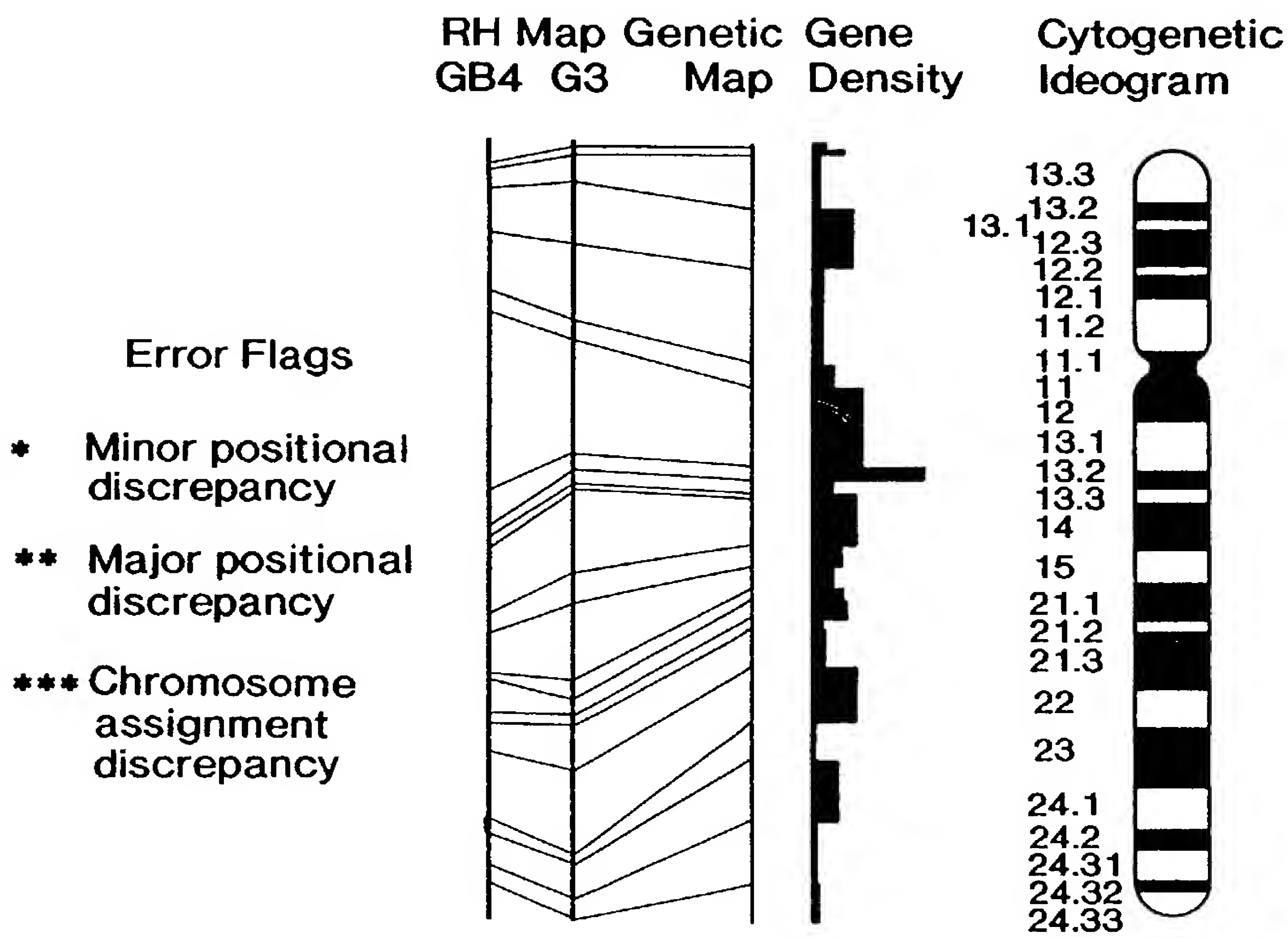
FIG. 2H

	475.18	P>3.00		WI-22211		Homo sapiens full length insert cDNA clone..
	475.18	P2.08		stSG48093		ESTs
	475.18	"		A004P27		ESTs, Weakly similar to MULTIDRUG RESI..
	475.35	P2.10		stSG9904		ESTs
	475.40	P0.45		sts-AA024696		ESTs
	475.51	P>3.00		stSG53793		ESTs
	476.10	P>3.00		Bda98d05		Homo sapiens full length insert cDNA clone..
	476.21	P>3.00		sts-H24468		ESTs
	476.21	P>3.00		sts-N94741		ESTs
	476.64	P0.28		stSG22488		ESTs
	476.85	P0.36		stSG44909		ESTs
	477.06	P0.10		stSG54797		ESTs
	477.27	P1.33		stSG48099		ESTs
	477.37	P0.09	*	sts-AA028894		Homo sapiens silencing mediator of retinoic..
	477.80	P1.44		stSG52727		EST
	477.80	"		U44799		Human U1-snRNP binding protein homolog mR..
	477.80	"		WI-15963		ESTs
	477.80	"		stSG53886		ESTs, Weakly similar to neuronal thread pr..
	478.74	P0.01		WIAF-364		ESTs
	479.01	P0.21		WI-21080		ESTs
	479.13	P0.19		A009B29		ESTs
	479.33	P0.22		A006F32	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33	P0.19		WIAF-449	EIF2B1	eukaryotic translation initiation factor 2B..
	479.33	P0.19	*	WI-15890		H.sapiens mRNA for transmembrane protein r..
	479.55	P0.20	*	stSG349		H.sapiens mRNA for transmembrane protein r..
	479.55	"	*	A004O46	BDKRB2	bradykinin receptor B2
	479.55	"		stSG42540		ESTs
	479.55	"		sts-N26791		ESTs
	479.55	"		stSG53943		ESTs
	479.55	"		stSG49468		EST
145.7	479.74	P0.16		AFM294ze9	D12S342	Microsatellite marker AFM294ze9
	481.46	P0.00		sts-AA007694		EST
147.5	◆ 481.56	F		AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1

Next interval down

FIG. 2I

Chromosome 12: D12S340–D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S340 (147.5 cM)
Bottom of interval:	D12S97 (160.9 cM)
Genetic size of bin:	13 cM
Physical size of bin:	13 cR_{3000}

↑ Next interval up

147.5 ◆	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
	481.66 P0.00	SGC31838		ESTs
	483.18 P0.70	stSG48255		ESTs
	483.58 P0.69	stSG47315		ESTs

FIG. 2J

483.87	P0.83		stSG47707		ESTs
484.70	P0.93		stSG4060		ESTs
484.70	"		stSG62390	GTF2H3	general transcription factor IIH, polypepti..
484.70	"		stSG42994		ESTs
484.73	P0.74		stSG46906		ESTs
484.80	P0.91		A004X33		ESTs
484.91	P1.11		stSG3211		ESTs, Weakly similar to B-cell growth fact..
484.91	"	*	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91	"	*	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91	"		sts-T58259		ESTs, Weakly similar to B-cell growth fact..
484.91	"		stSG52737		ESTs
484.91	"		Bda03b10	UBC	ubiquitin C
484.91	"		stSG1936	CD36L1	CD36 antigen (collagen type I receptor, thr..
484.91	"		sts-AA017225		ESTs
484.91	P1.15		WI-12212		ESTs
485.12	P1.18		A004F14		ESTs
485.12	P1.18		SGC31333		ESTs
485.23	P1.21	*	WI-12482	BDKRB2	bradykinin receptor B2
485.23	P1.07		sts-AA017698		ESTs
485.33	P1.22		WI-12422		ESTs
485.51	P1.18		stSG42398		EST
485.64	P1.04		sts-AA009669		ESTs
486.07	P2.50		stSG21539		EST
486.13	P1.44		WI-12439		EST
486.34	P1.26		sts-W31616	UBC	ubiquitin C
486.38	P>3.00		stSG54715		ESTs
486.76	P1.64	*	WI-6921		H.sapiens mRNA for transmembrane protein r..
487.08	P>3.00		WI-13120		Human mRNA for KIAA0318 gene, partial cds
487.23	P>3.00		stSG54353		ESTs
487.23	P>3.00		stSG22703		EST
487.28	P>3.00		stSG62698		ESTs
487.28	P>3.00	*	sts-D60472		Homo sapiens silencing mediator of retinoic..
487.28	P>3.00		stSG36097		ESTs
487.33	P1.36		sts-U37146		Homo sapiens silencing mediator of retinoic..

FIG. 2K

		487.50	P>3.00		stSG9807		ESTs
		487.50	P>3.00		stSG15434		ESTs
		487.60	P>3.00		stSG53251		ESTs
		487.60	P>3.00		stSG30525	SRRP129	SC35-interacting protein 1
		487.60	P>3.00		stSG46424		ESTs
		487.70	P>3.00		A007A34		ESTs
154.4		487.75	P2.00		AFMa197zd9	D12S1609	Microsatellite marker AFMa197zd9
		487.75	P2.02		A006D44		ESTs
		487.80	P>3.00		SGC30248		ESTs, Weakly similar to peptide/histidine ..
		488.07	P1.68		stSG6320		Homo sapiens clone 24617 mRNA sequence
		488.07	P1.66		stSG6305		Homo sapiens clone 24790 mRNA sequence
		488.07	P0.02		sts-N20163		Homo sapiens full length insert cDNA clone..
		488.12	P>3.00		stSG60065		ESTs
		488.12	P>3.00		stSG47723		ESTs
		488.44	P1.59		stSG3292		Homo sapiens clone 24790 mRNA sequence
		488.44	P0.03		WIAF-856		EST, Weakly similar to reverse transcripta..
		488.65	P1.54		WI-12272		Homo sapiens clone 24790 mRNA sequence
		488.65	P1.82		stSG52343		ESTs
		488.82	P1.80		stSG16387	CPN2	carboxypeptidase N, polypeptide 2, 83kD
		488.97	P1.80		SGC31722		ESTs
		489.07	P0.06		stSG54325		ESTs
		489.07	P>3.00		stSG63473		ESTs
160.9	◆	489.07	P>3.00		AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1
		489.14	P0.17		sts-T81113		ESTs
		489.29	P0.05		sts-AA025438		EST
		489.50	P1.37	***	Cda1ad08		ESTs
		489.50	P0.05		WI-15018		ESTs
		489.50	P1.50		WI-18492		ESTs
		489.57	P1.48		WI-16177		Homo sapiens androgen receptor associated p..
		489.67	P1.44		stSG53307		ESTs
		489.71	P1.43		stSG53541		Homo sapiens hiwi mRNA, partial cds
		489.71	P1.43		stSG9546		Homo sapiens clone 24617 mRNA sequence
		489.89	P1.56		A006O16		ESTs
		490.10	P1.42		H64839		EST

FIG. 2L

	490.20	P0.05	stSG43910	SFRS8	splicing factor, arginine/serine-rich 8 (sup..
160.9	◆ 494.19	F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6

Next interval down

FIG. 2M

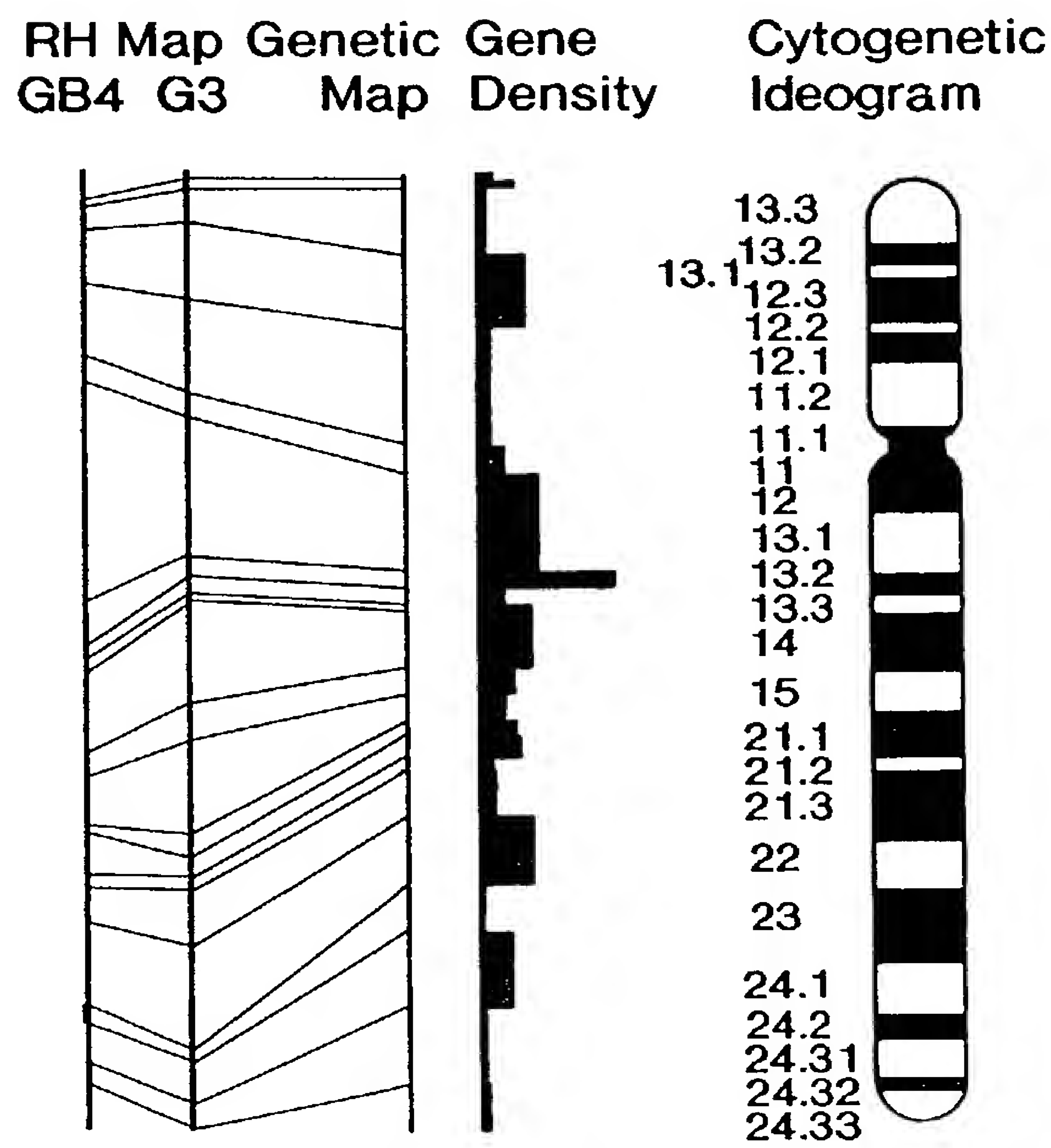
Chromosome 12: D12S97–qTEL

Error Flags

* Minor positional discrepancy

** Major positional discrepancy

*** Chromosome assignment discrepancy



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval:	D12S97 (160.9 cM)
Bottom of interval:	chr12_qTEL (169.1 cM)
Genetic size of bin:	8 cM
Physical size of bin:	172 cR_{3000}

↑ Next interval up

160.9	◆ 494.19	F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
	498.06	P0.02	stSG53600		ESTs, Weakly similar to peptide/histidine ..
	499.71	P1.73	stSG3357		ESTs
165.7	499.71	"	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2N

499.71	P1.72	stSG30906		ESTs
499.71	"	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71	P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92	P>3.00	stSG43769		ESTs
500.50	P1.88	stSG26056		ESTs
500.50	P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61	P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61	"	sts-N59820		ESTs
500.61	"	stSG42115	KIAA0331	KIAA0331 gene product
500.61	"	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61	"	stSG52521		ESTs
500.61	"	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61	"	AA252357		ESTs
500.61	"	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61	"	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61	P>3.00	stSG31443		ESTs
500.61	P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61	P2.49	stSG50559		ESTs
501.04	P1.10	stSG54842		ESTs
501.04	P2.03	A008Y05		Unknown
501.89	P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99	P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99	P>3.00	sts-H94865		EST
501.99	P>3.00	R50113		ESTs
502.10	P1.75	stSG48386		ESTs
502.10	"	stSG50504		ESTs
502.63	P0.06	A006R19		ESTs
502.63	P1.06	WIAF-864		ESTs
502.94	P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04	P1.42	A004B47		ESTs, Highly similar to DNA polymerase ep..
503.25	P0.28	stSG27206		ESTs
503.25	"	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46	P0.23	stSG8935		ESTs
504.68	P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

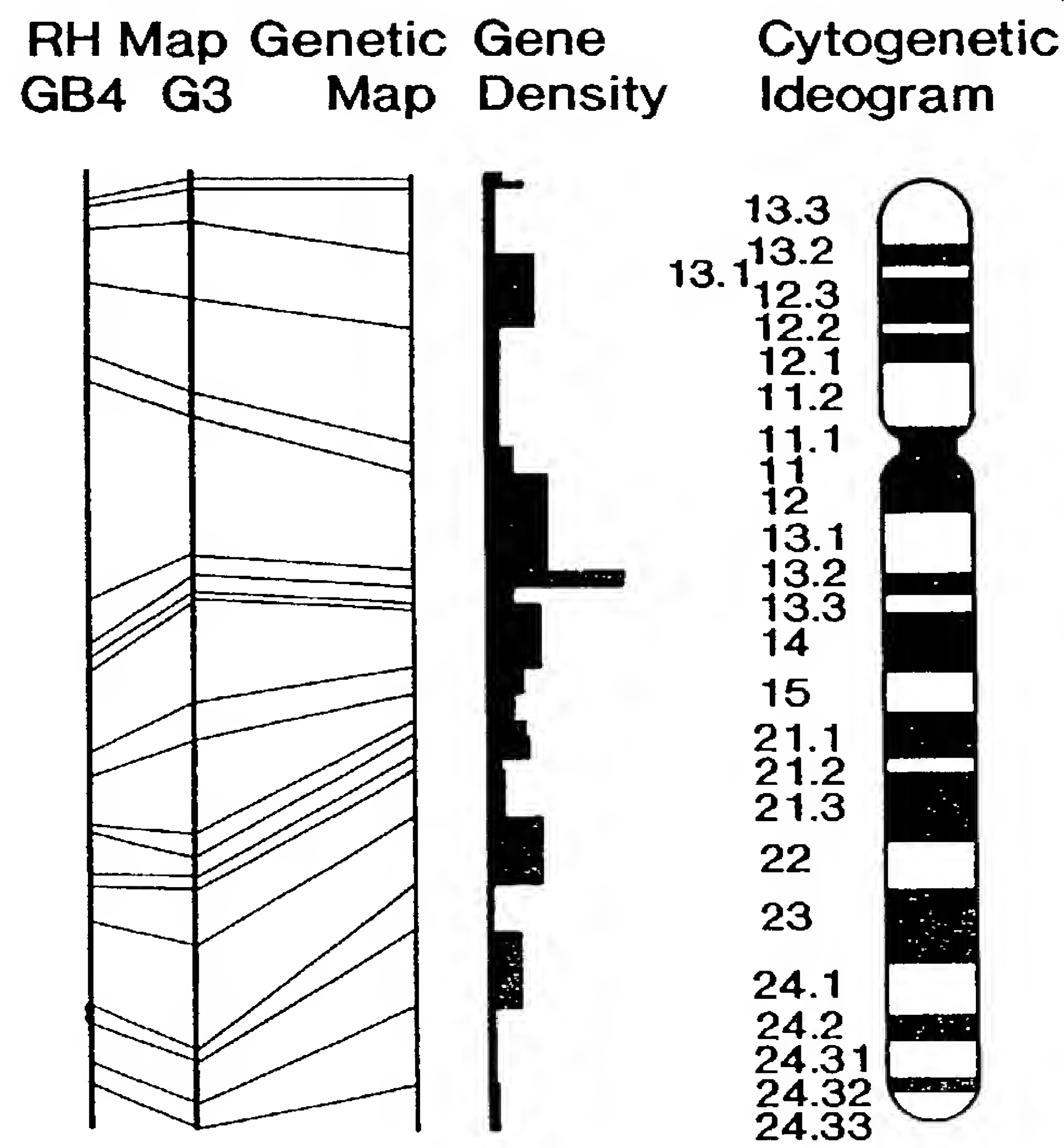
FIG. 2O

		504.68	"		A005Q05		ESTs
		504.68	"		stSG8142		ESTs, Highly similar to DNA polymerase ep..
169.1		506.39	F		AFM310vd5	D12S357	Microsatellite marker AFM310vd5
		506.39	P0.02		A005X42		Homo sapiens mRNA for KIAA0692 protein, p..
		508.59	P0.78		Cda18g06		ESTs
	◆	508.59	P0.78	**	Cda1jf08		Homo sapiens mRNA for GCP170, complete cd..
		508.59	P0.54		R39599		ESTs
		509.98	P0.10		stSG31494	ZNF140	zinc finger protein 140 (clone pHZ-39)
		509.98	P0.16		stSG40222		ESTs
		509.98	"		sts-R55615		ESTs, Weakly similar to zinc finger protei..
		509.98	"		sts-R02295		ESTs
		509.98	"		sts-R81342		ESTs
		511.20	F		TEL-12q82		Marker TEL-12q82
		512.81	P0.20		sts-H65839		ESTs, Weakly similar to transformation-rel..
		514.97	P0.36		stSG46141		ESTs, Weakly similar to zinc finger protei..
		514.97	P0.90		stSG52998		ESTs
		519.10	P1.77		A008W21	CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
		519.54	P0.81		stSG52716		ESTs

TELOMERE

FIG. 2P

Chromosome 12: D12S79–D12S366



Error Flags

* Minor positional discrepancy

** Major positional discrepancy

*** Chromosome assignment discrepancy

The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval:	D12S79 (126.1 cM)
Bottom of interval:	D12S366 (133.8 cM)
Genetic size of bin:	8 cM
Physical size of bin:	63 cR_{10000}

FIG. 3A

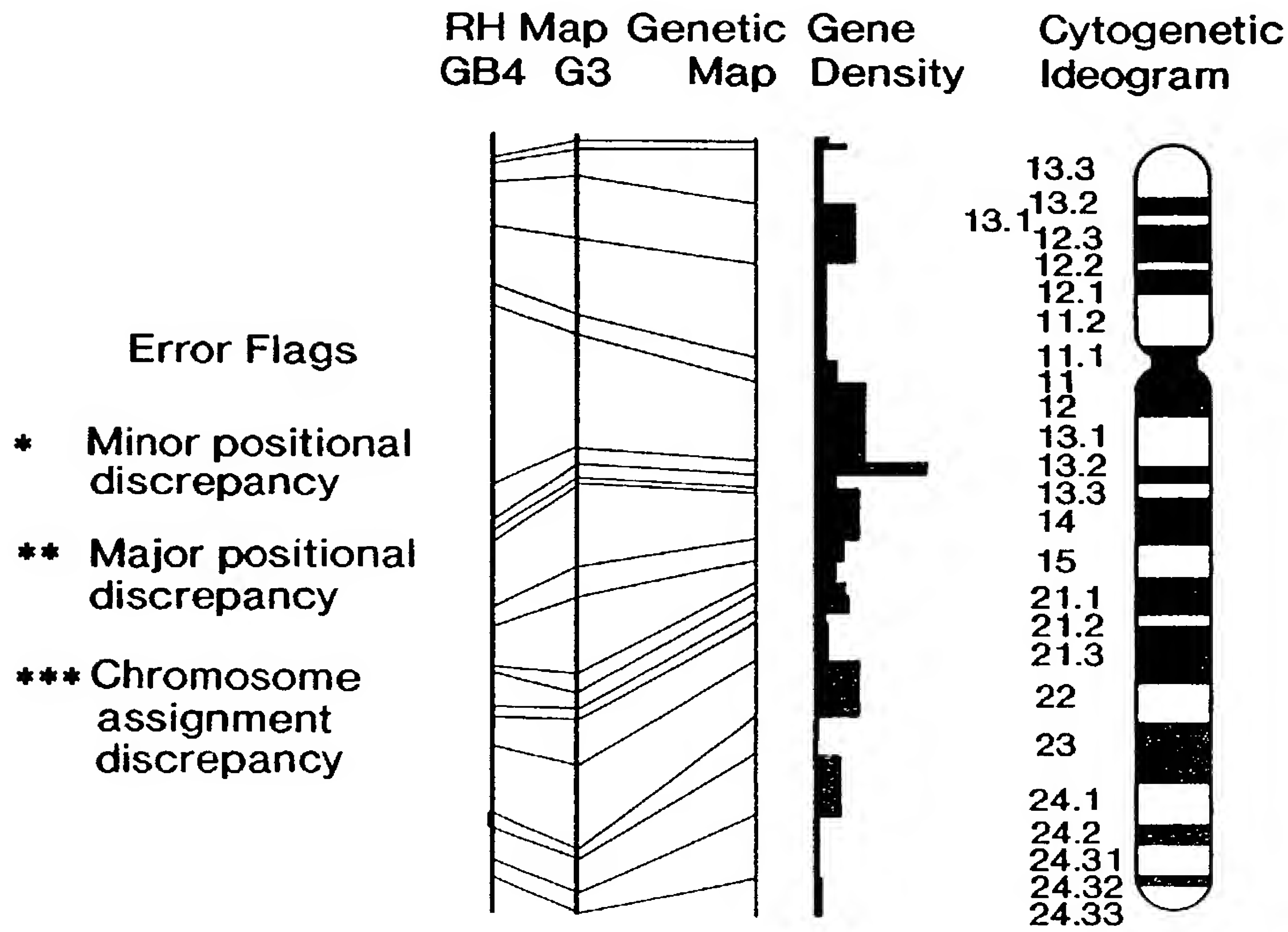
Next interval up

126.1	◆ 4955	F		AFM067yc5	D12S79	Microsatellite anchor marker AFM067yc5 (SHGC-692)
129.2	4988	F		AFMa067we1	D12S1718	Microsatellite marker AFMa067we1 (SHGC-20..
	◆ 5007	F	*	SHGC-2657		Homo sapiens clone 23714 mRNA sequence
	◆ 5014	F	*	SHGC-2653		Homo sapiens clone 23714 mRNA sequence
133.8	◆ 5018	F		AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)

Next interval down

FIG. 3B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval:	D12S366 (133.8 cM)
Bottom of interval:	D12S340 (147.5 cM)
Genetic size of bin:	14 cM
Physical size of bin:	261 cR_{10000}

FIG. 3C

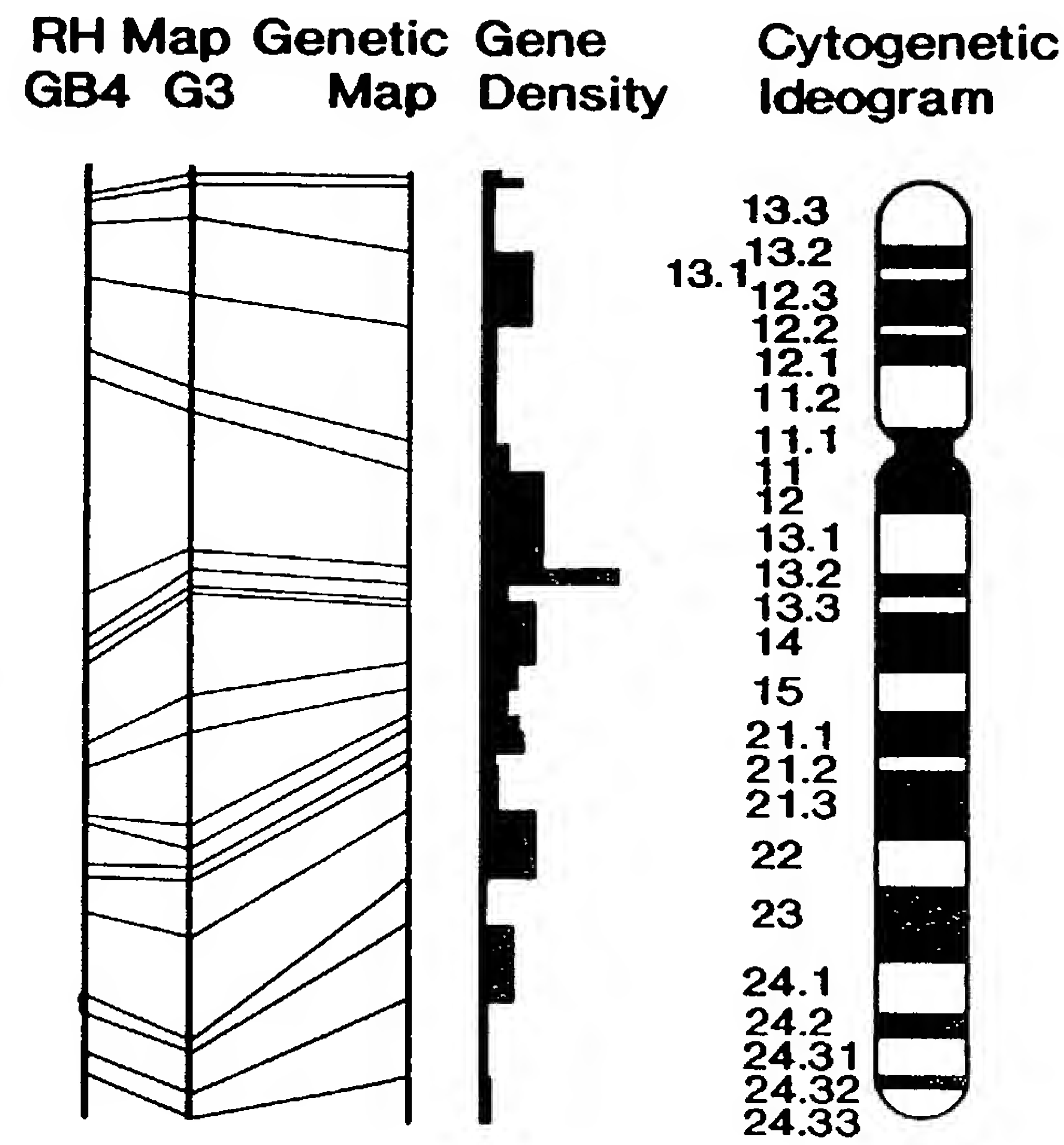
↑ Next interval up

133.8	◆ 5018	F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047	F	AFMa225xe5	D12S1619	Microsatellite marker AFMa225xe5 (SHGC-20..
	◆ 5085	F	SHGC-33949	KIAA0262	KIAA0262 gene product
	◆ 5089	F	SHGC-10488	KIAA0152	KIAA0152 gene product
	◆ 5093	F	SHGC-10346		Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098	F	SHGC-13898		Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163	F	AFM220zf4	D12S321	Microsatellite marker AFM220zf4 (SHGC-212..
	5199	F	SHGC-11702		ESTs
147.5	◆ 5279	F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)

↓ Next interval down

FIG. 3D

Chromosome 12: D12S340-D12S97



Error Flags

* Minor positional discrepancy

** Major positional discrepancy

*** Chromosome assignment discrepancy

The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

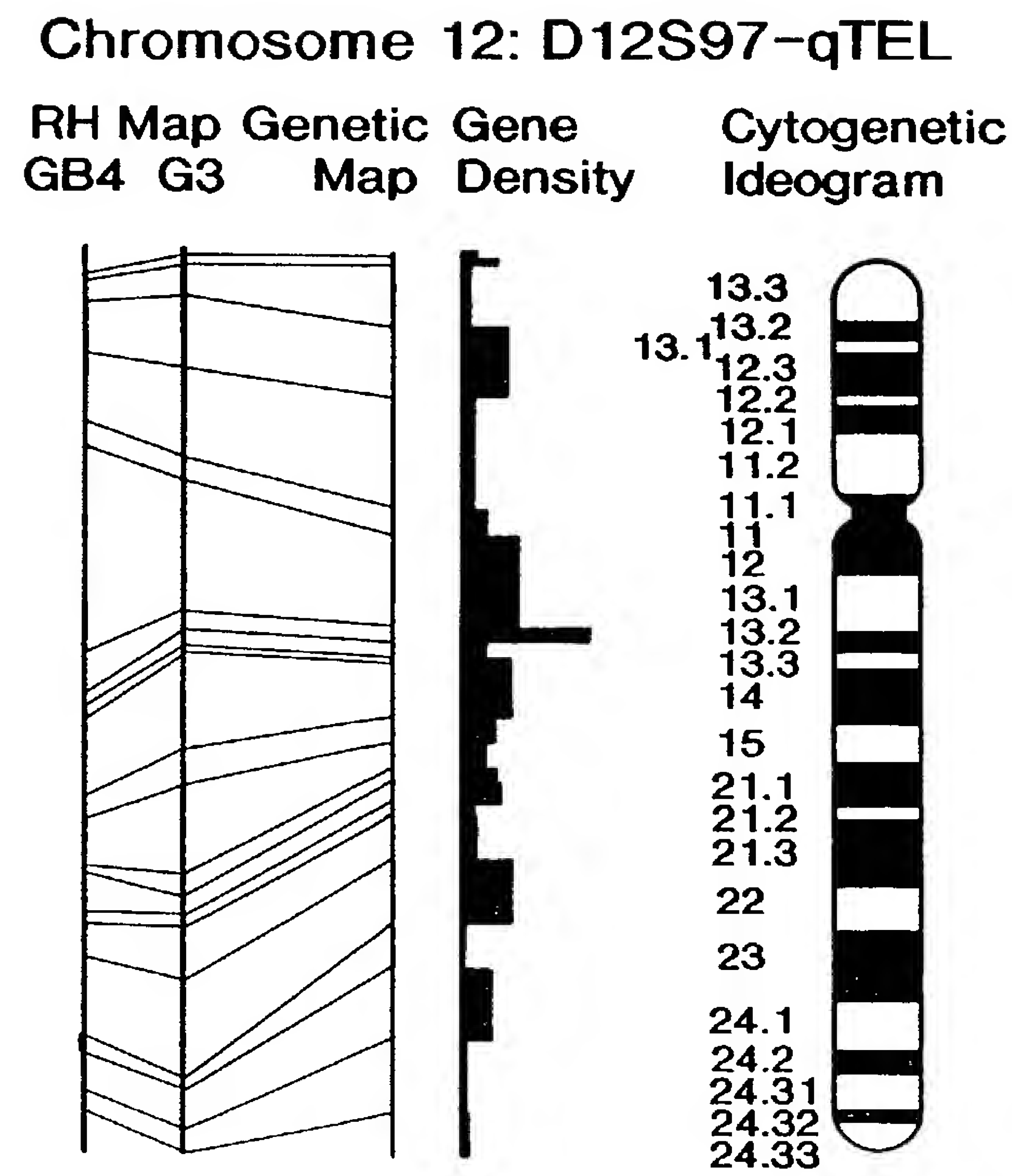
Top of interval:	D12S340 (147.5 cM)
Bottom of interval:	D12S97 (160.9 cM)
Genetic size of bin:	13 cM
Physical size of bin:	151 cR_{10000}

FIG. 3E

↑ Next interval up

147.5	◆ **5279**	**F**	**AFM294xgl**	**D12S340**	**Microsatellite anchor marker AFM294xgl (SHGC-2134)**
148.3	5288	F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..
154.4	5316	F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..
149.5	5358	F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..
157.2	5393	F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..
160.9	◆ 5415	F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..
160.9	◆ **5430**	**F**	**AFM210zd6**	**D12S97**	**Microsatellite anchor marker AFM210zd6 (SHGC-372)**

FIG. 3F



Error Flags

* Minor positional discrepancy

** Major positional discrepancy

*** Chromosome assignment discrepancy

The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval:	D12S97 (160.9 cM)
Bottom of interval:	chr12_qTEL (169.1 cM)
Genetic size of bin:	8 cM
Physical size of bin:	~ 4429 cR_{10000}

Next interval up

160.9 ◆ 5430 F AFM210zd6 D12S97 Microsatellite anchor marker AFM210zd6 (SHGC-372)

TELOMERE

FIG. 3G

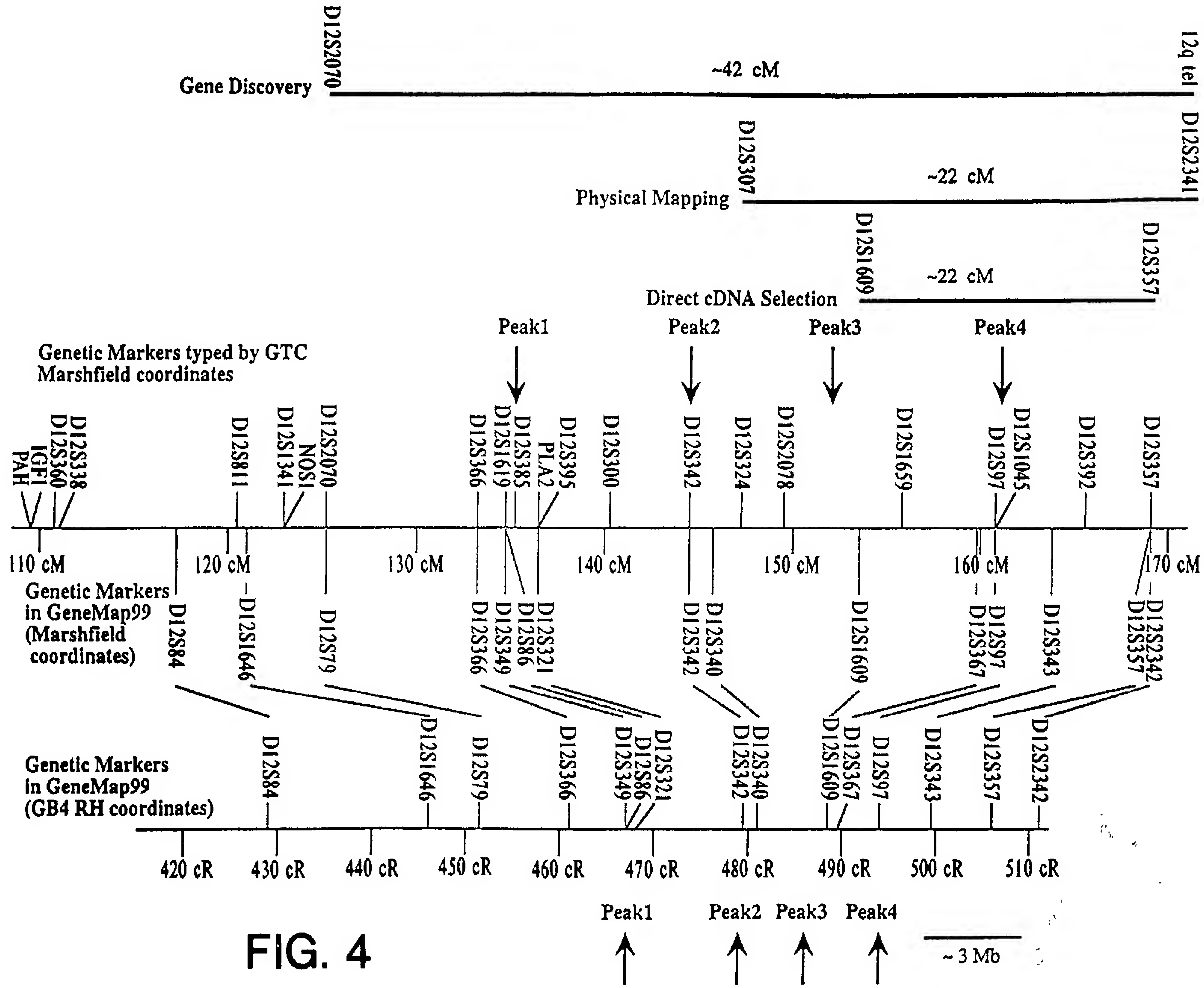
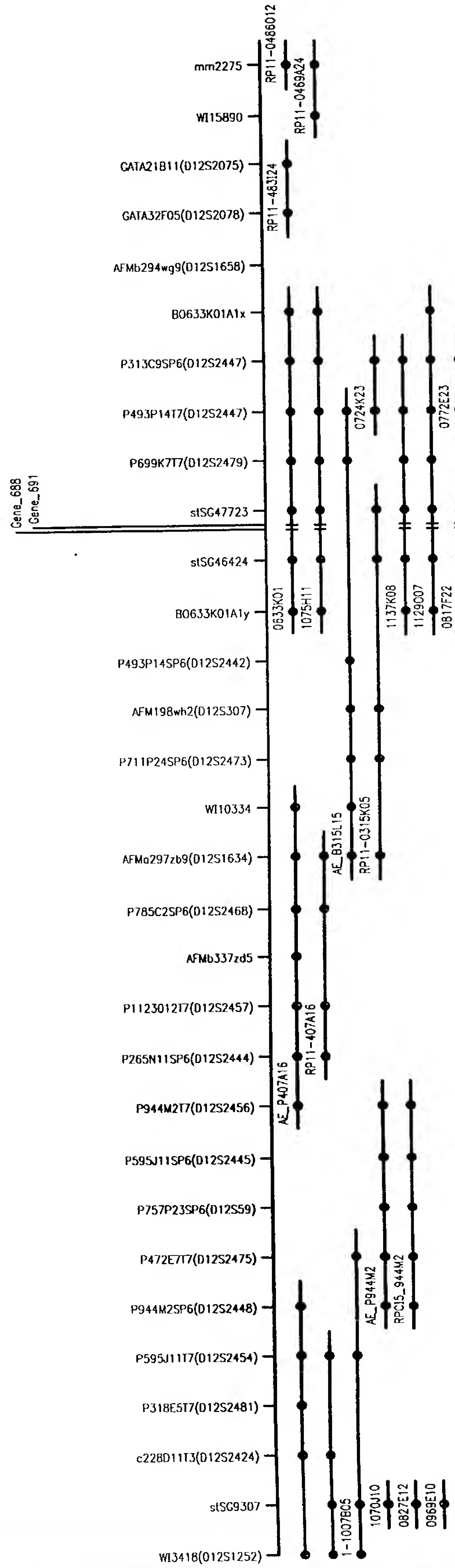
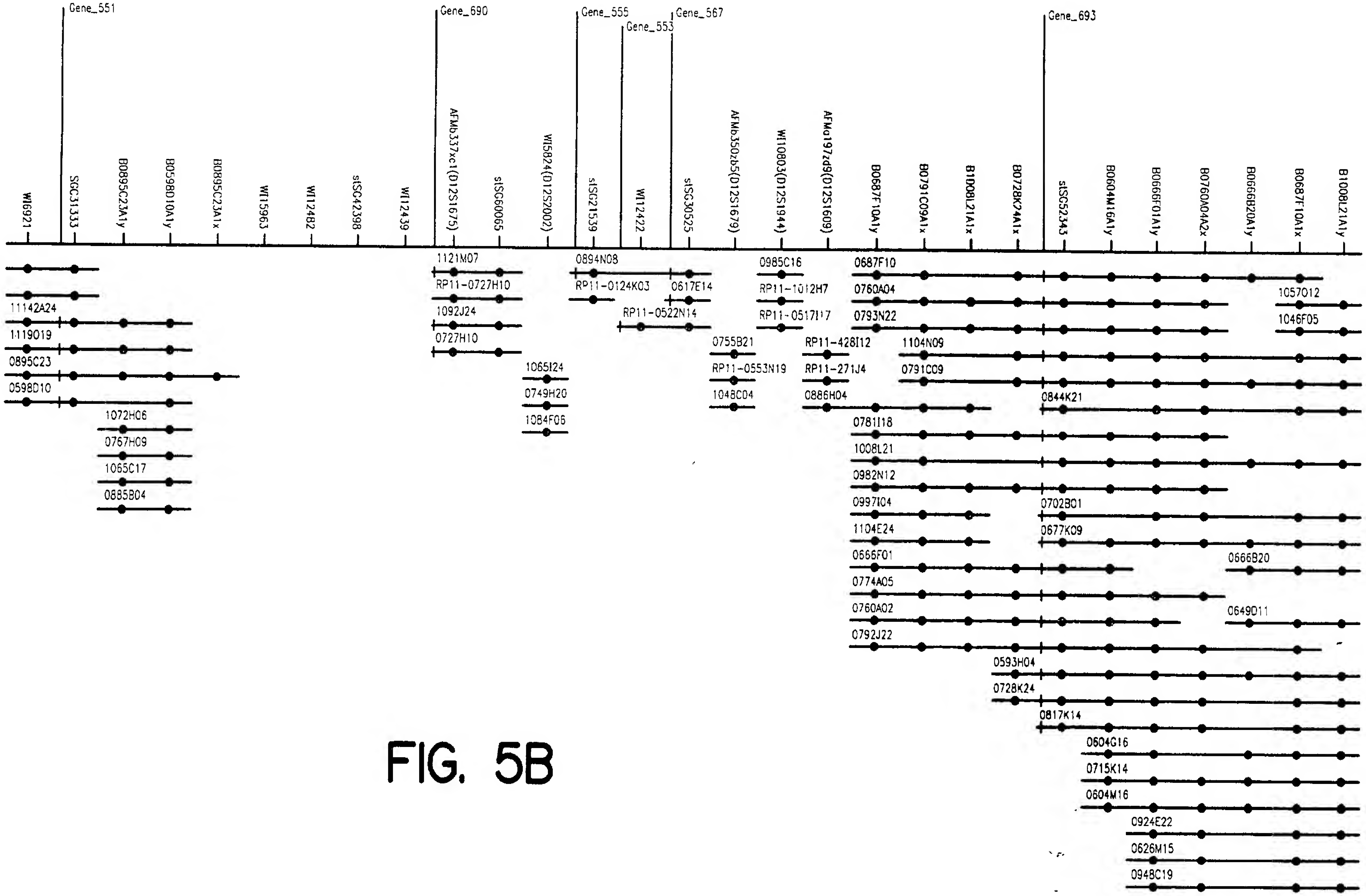

Gene Discovery
D12S2070
~42 cM
12q tel
Physical Mapping
D12S307
~22 cM
D12S2341
Direct cDNA Selection
D12S1609
~22 cM
D12S357
Peak1
Peak2
Peak3
Peak4
Genetic Markers typed by GTC Marshfield coordinates
PAH
IGF1
D12S360
D12S338
D12S811
D12S1341
NOS1
D12S2070
D12S366
D12S1619
D12S385
PLA2
D12S395
D12S300
D12S342
D12S324
D12S2078
D12S1659
D12S97
D12S1045
D12S392
D12S357
110 cM
120 cM
130 cM
140 cM
150 cM
160 cM
170 cM
Genetic Markers in GeneMap99 (Marshfield coordinates)
D12S84
D12S1646
D12S79
D12S366
D12S349
D12S86
D12S321
D12S342
D12S340
D12S1609
D12S367
D12S97
D12S343
D12S357
D12S2342
Genetic Markers in GeneMap99 (GB4 RH coordinates)
D12S84
D12S1646
D12S79
D12S366
D12S349
D12S86
D12S321
D12S342
D12S340
D12S1609
D12S367
D12S97
D12S343
D12S357
D12S2342
420 cR
430 cR
440 cR
450 cR
460 cR
470 cR
480 cR
490 cR
500 cR
510 cR
Peak1
Peak2
Peak3
Peak4
~ 3 Mb

FIG. 4



mm2275
WI15890
GATA21B11(D12S2075)
GATA32F05(D12S2078)
AFMb294wg9(D12S1658)
B0633K01A1x
P313C9SP6(D12S2447)
P493P14T7(D12S2447)
P699K7T7(D12S2479)
stSG47723
stSG46424
B0633K01A1y
P493P14SP6(D12S2442)
AFM198wh2(D12S307)
P711P24SP6(D12S2473)
WI10334
AFMa297zb9(D12S1634)
P785C2SP6(D12S2468)
AFMb337zd5
P1123O12T7(D12S2457)
P265N11SP6(D12S2444)
P944M2T7(D12S2456)
P595J11SP6(D12S2445)
P757P23SP6(D12S59)
P472E7T7(D12S2475)
P944M2SP6(D12S2448)
P595J11T7(D12S2454)
P318E5T7(D12S2481)
c228D11T3(D12S2424)
stSG9307
WI3418(D12S1252)
Gene_688
Gene_691
RP11-0486O12
RP11-0469A24
RP11-483I24
0633K01
1075H11
0724K23
1137K08
1129O07
0817F22
0772E23
0633O01
1141G08
0779H09
0727N11
0873P03
RP11-0983C02
0983C02
0793F21
AE_B315L15
RP11-0315K05
AE_P407A16
RP11-407A16
AE_P944M2
RPCI5_944M2
1-1007B05
1070J10
0827E12
0969E10

FIG. 5A



Gene_551
Gene_690
Gene_555
Gene_553
Gene_567
Gene_693
WI6921
SGC31333
B0895C23A1y
B0598D10A1y
B0895C23A1x
WI15963
WI12482
stSG42398
WI12439
AFMb337xc1(D12S1675)
stSG60065
WI5824(D12S2002)
stSG21539
WI12422
stSG30525
AFMb350zb5(D12S1679)
WI10803(D12S1944)
AFMa197zd9(D12S1609)
B0687F10A1y
B0791C09A1x
B1008L21A1x
B0728K24A1x
stSG52343
B0604M16A1y
B0666F01A1y
B0760A04A2x
B0666B20A1y
B0687F10A1x
B1008L21A1y
1142A24
1119O19
0895C23
0598D10
1072H06
0767H09
1065C17
0885B04
1121M07
RP11-0727H10
1092J24
0727H10
1065I24
0749H20
1084F06
0894N08
RP11-0124K03
0617E14
RP11-0522N14
0755B21
RP11-0553N19
1048C04
0985C16
RP11-1012H7
RP11-0517I17
RP11-428I12
RP11-271J4
0886H04
0687F10
0760A04
0793N22
1104N09
0791C09
0781I18
1008L21
0982N12
0997I04
1104E24
0666F01
0774A05
0760A02
0792J22
0844K21
0702B01
0677K09
0593H04
0728K24
0817K14
0604G16
0715K14
0604M16
0924E22
0626M15
0948C19
0666B20
0649D11
1057O12
1046F05

FIG. 5B

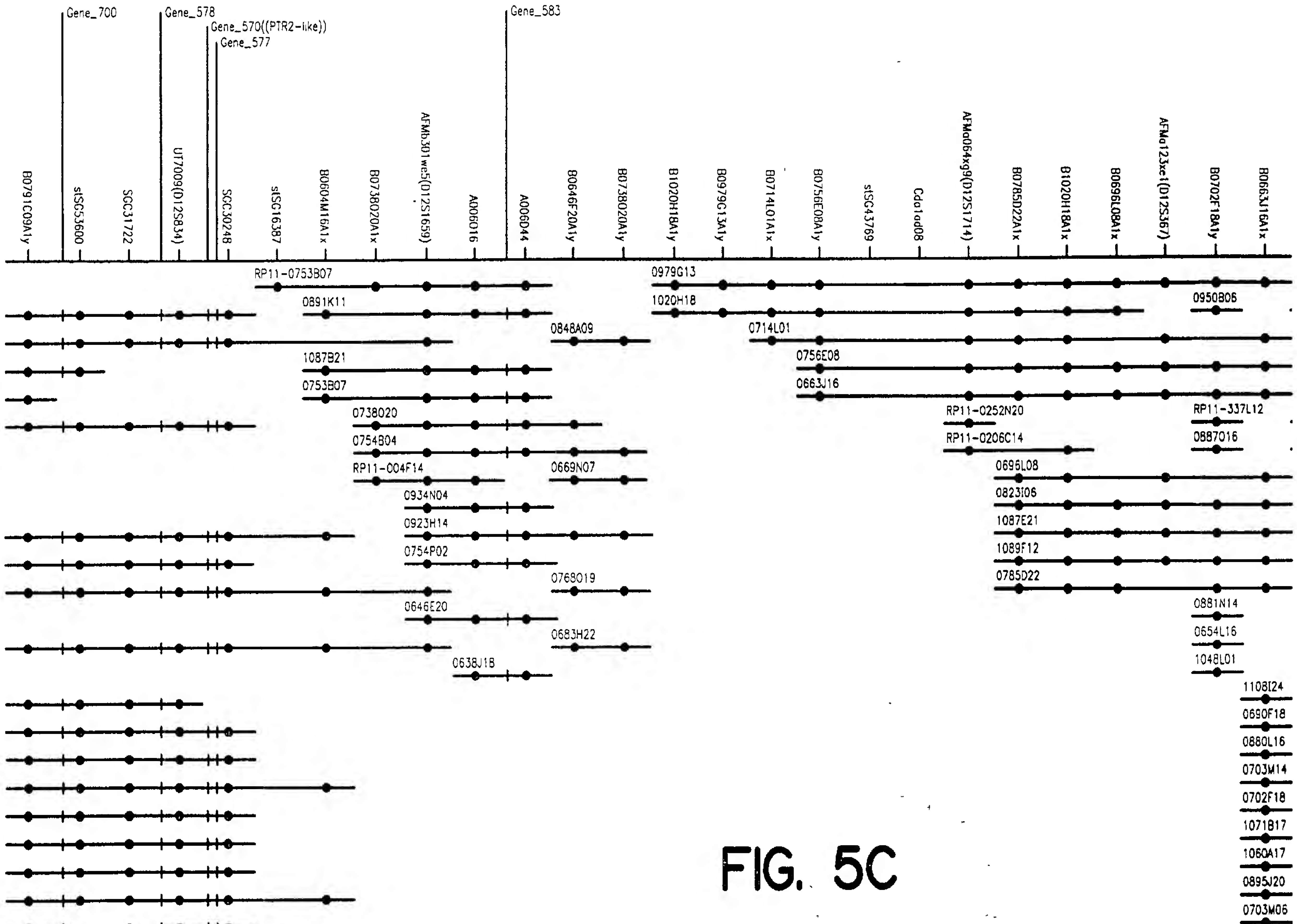

Gene_700
Gene_578
Gene_570((PTR2-like))
Gene_577
Gene_583
B0791C09A1y
stSG53600
SGC31722
UT7009(D12S834)
SGC30248
stSG16387
B0604M16A1x
B0738020A1x
AFMb301we5(D12S1659)
A006016
A006D44
B0646F20A1y
B0738020A1y
B1020H18A1y
B0979G13A1y
B0714L01A1x
B0756E08A1y
stSG43769
Cda1ad08
AFMa064xg9(D12S1714)
B0785D22A1x
B1020H18A1x
B0696L08A1x
AFMa123xe1(D12S367)
B0702F18A1y
B0663J16A1x
RP11-0753B07
0891K11
1087B21
0753B07
0738020
0754B04
RP11-004F14
0934N04
0923H14
0754P02
0646E20
0638J18
0848A09
0669N07
0768019
0683H22
0979G13
1020H18
0714L01
0756E08
0663J16
RP11-0252N20
RP11-0206C14
0696L08
0823I06
1087E21
1089F12
0785D22
0950B06
RP11-337L12
0887016
0881N14
0654L16
1048L01
1108I24
0690F18
0880L16
0703M14
0702F18
1071B17
1060A17
0895J20
0703M06

FIG. 5C

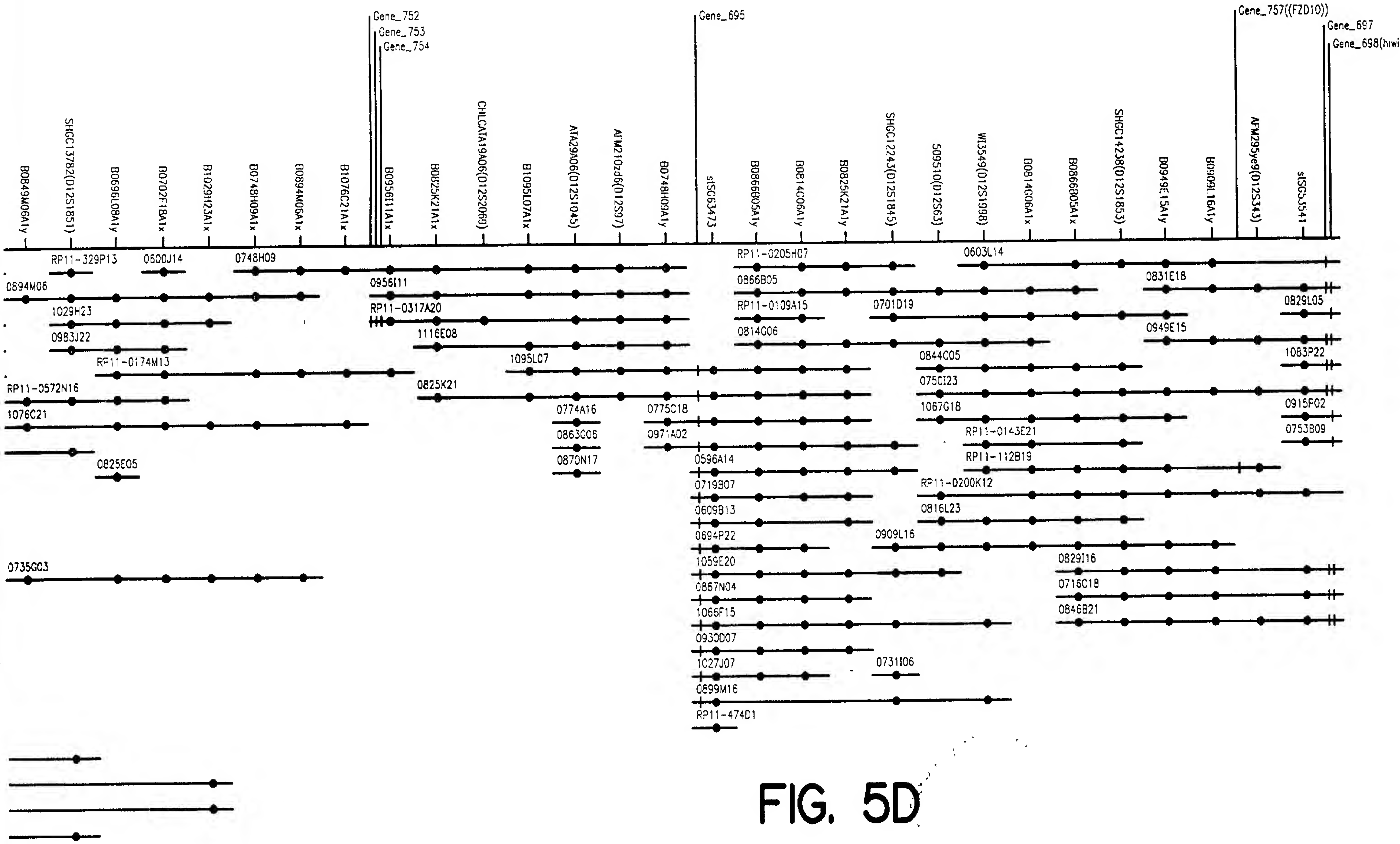

Gene_752
Gene_753
Gene_754
Gene_695
Gene_757((FZD10))
Gene_697
Gene_698(hiwi)
B0849M06A1y
SHGC13782(D12S1851)
B0696L08A1y
B0702F18A1x
B1029H23A1x
B0748H09A1x
B0894M06A1x
B1076C21A1x
B0956I11A1x
B0825K21A1x
CHLCATA19A06(D12S2069)
B1095L07A1x
ATA29A06(D12S1045)
AFM210zd6(D12S97)
B0748H09A1y
stSG63473
B0866B05A1y
B0814G06A1y
B0825K21A1y
SHGC12243(D12S1845)
509510(D12S63)
WI3549(D12S1998)
B0814G06A1x
B0866B05A1x
SHGC14238(D12S1853)
B0949E15A1y
B0909L16A1y
AFM295ye9(D12S343)
stSG53541
RP11-329P13
0600J14
0748H09
0894M06
1029H23
0983J22
RP11-0174M13
RP11-0572N16
1076C21
0825E05
0735G03
0956I11
RP11-0317A20
1116E08
1095L07
0825K21
0774A16
0863G06
0870N17
0775C18
0971A02
RP11-0205H07
0866B05
RP11-0109A15
0814G06
0596A14
0719B07
0609B13
0694P22
1059E20
0867N04
1066F15
0930D07
1027J07
0899M16
RP11-474D1
0701D19
0603L14
0844C05
0750I23
1067G18
RP11-0143E21
RP11-112B19
RP11-0200K12
0816L23
0909L16
0731I06
0831E18
0949E15
0829I16
0716C18
0846B21
0829L05
1083P22
0915P02
0753B09

FIG. 5D

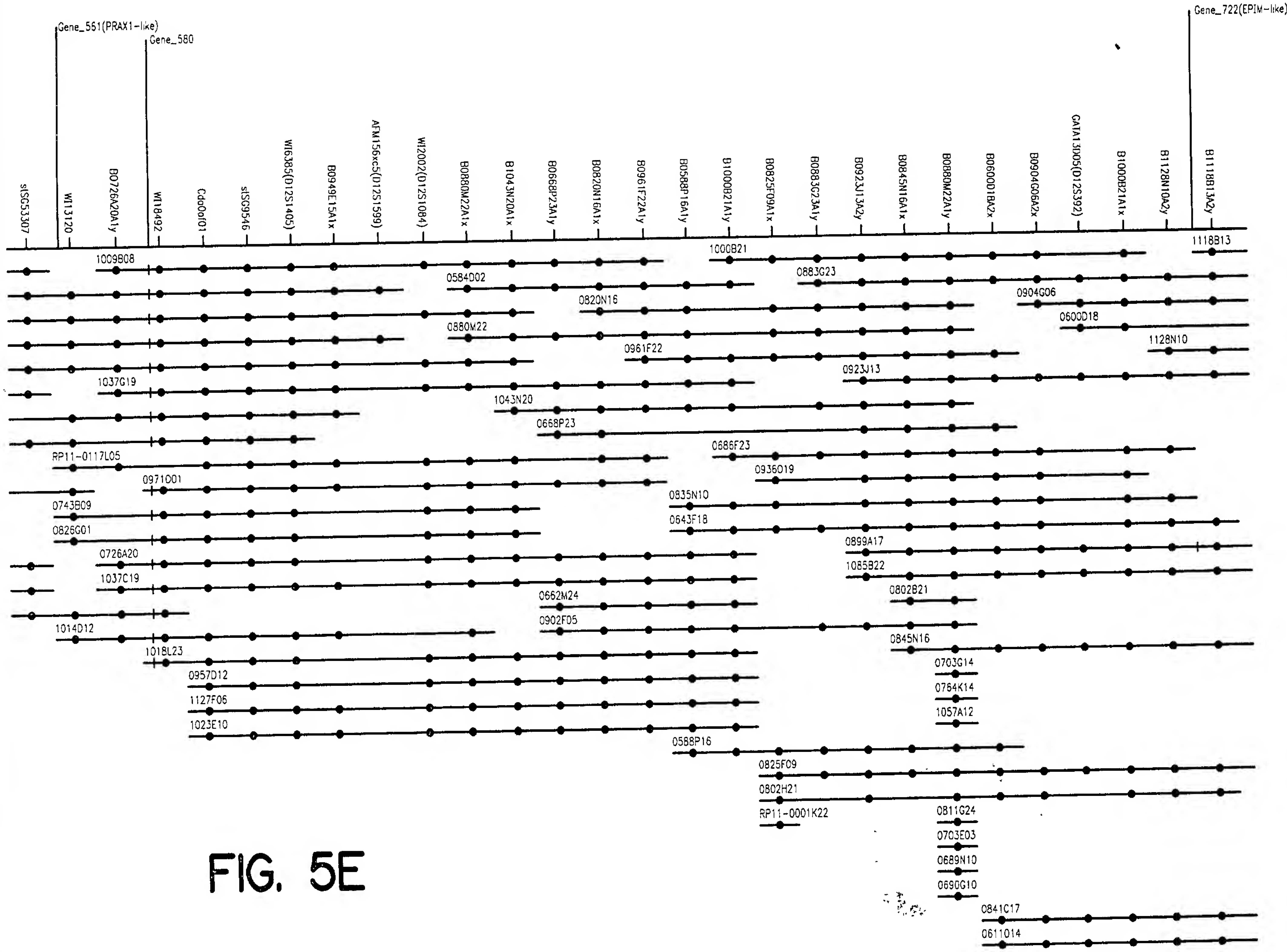

Gene_551(PRAX1-like)
Gene_580
Gene_722(EPIM-like)
stSG53307
WI13120
BO726A20A1y
WI18492
CdaOaf01
stSG9546
WI6385(D12S1405)
B0949E15A1x
AFM156xc5(D12S1599)
WI2002(D12S1084)
B0880M22A1x
B1043N20A1x
B0668P23A1y
B0820N16A1x
B0961F22A1y
B0588P16A1y
B1000B21A1y
B0825F09A1x
B0883G23A1y
B0923J13A2y
B0845N16A1x
B0880M22A1y
B0600D18A2x
B0904G06A2x
GATA13D05(D12S392)
B1000B21A1x
B1128N10A2y
B1118B13A2y
1118B13
1000B21
0883G23
0904G06
0600D18
1128N10
0923J13
1009B08
0584D02
0820N16
0880M22
0961F22
1037G19
1043N20
0668P23
0686F23
0936O19
RP11-0117L05
0971O01
0835N10
0643F18
0743B09
0826G01
0899A17
1085B22
0726A20
1037C19
0802B21
0662M24
0902F05
0845N16
1014D12
1018L23
0703G14
0764K14
1057A12
0957D12
1127F06
1023E10
0588P16
0825F09
0802H21
RP11-0001K22
0811G24
0703E03
0689N10
0690G10
0841C17
0611O14

FIG. 5E

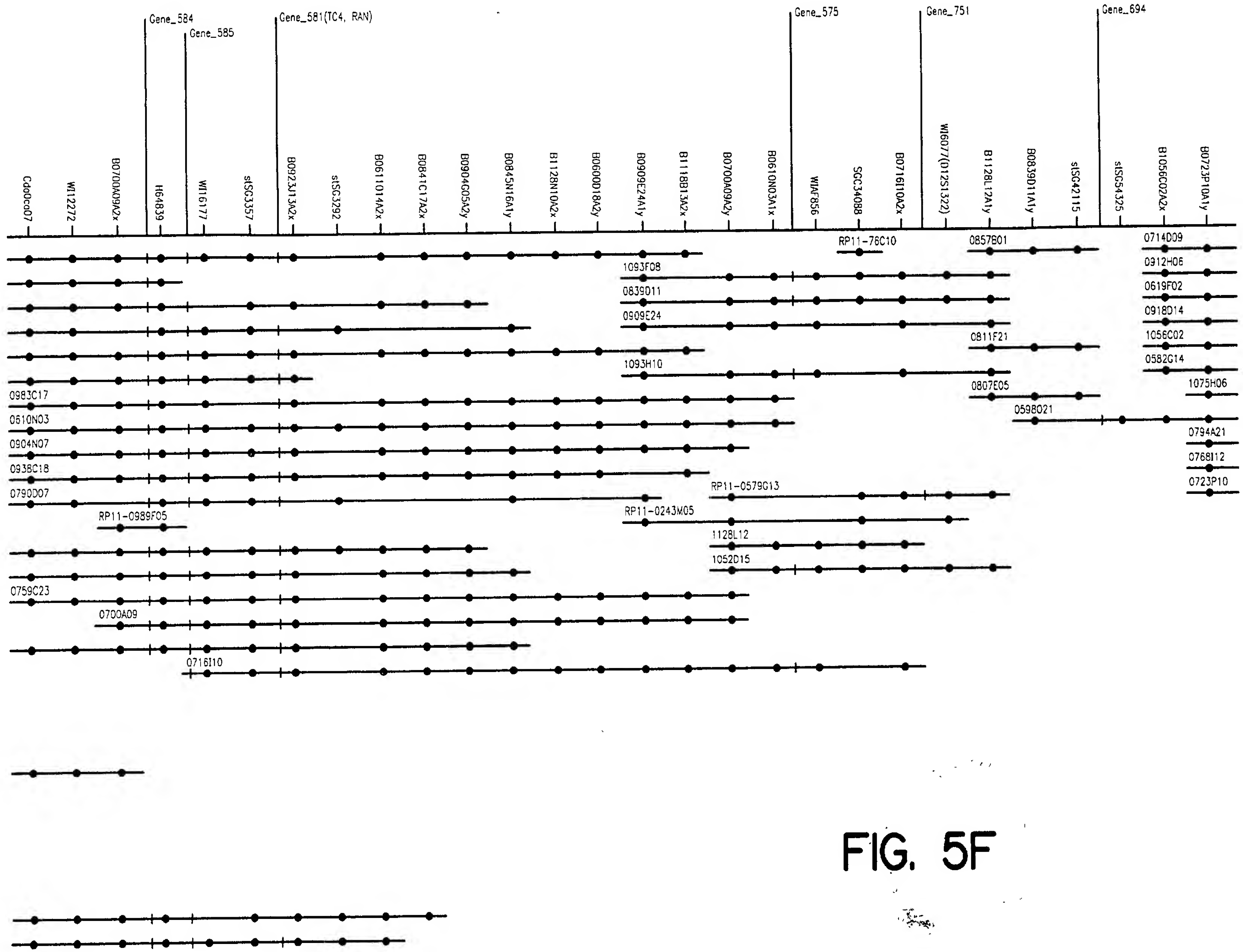

Gene_584
Gene_585
Gene_581(TC4, RAN)
Gene_575
Gene_751
Gene_694
Cda0ca07
WI12272
B0700A09A2x
H64839
WI16177
stSG3357
B0923J13A2x
stSG3292
B0611014A2x
B0841C17A2x
B0904G05A2y
B0845N16A1y
B1128N10A2x
B0600D18A2y
B0909E24A1y
B1118B13A2x
B0700A09A2y
B0610N03A1x
WIAF856
SGC34088
B0716I10A2x
WI6077(D12S1322)
B1128L12A1y
B0839D11A1y
stSG42115
stSG54325
B1056C02A2x
B0723P10A1y
RP11-76C10
0857B01
0714D09
0912H06
0619F02
0918D14
1056C02
0582G14
1075H06
1093F08
0839D11
0909E24
0811F21
1093H10
0807E05
0598O21
0794A21
0768I12
0723P10
0983C17
0610N03
0904N07
0938C18
0790D07
RP11-0579G13
RP11-0243M05
RP11-0989F05
1128L12
1052D15
0759C23
0700A09
0716I10

FIG. 5F

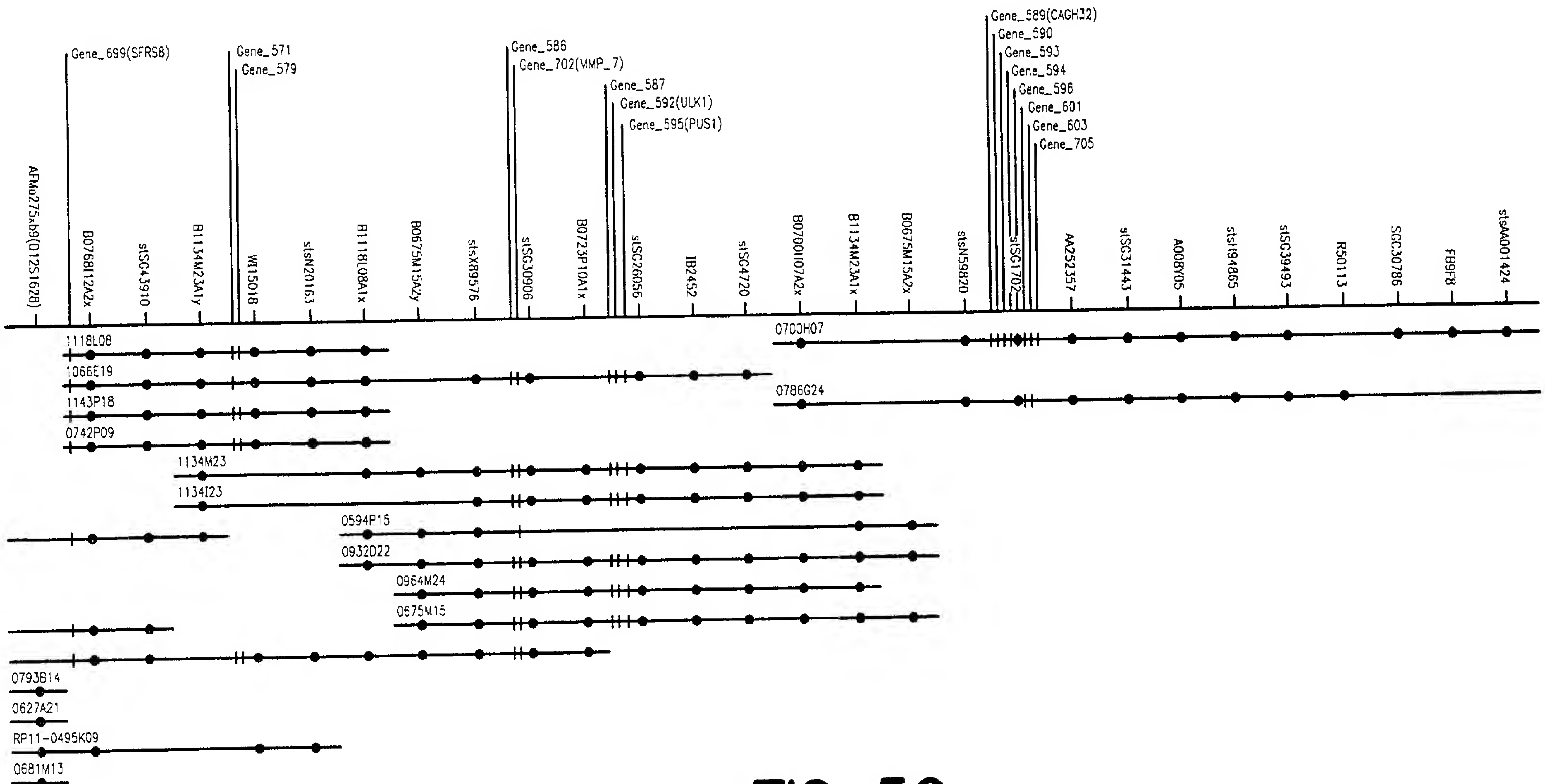

Gene_699(SFRS8)
Gene_571
Gene_579
Gene_586
Gene_702(MMP_7)
Gene_587
Gene_592(ULK1)
Gene_595(PUS1)
Gene_589(CAGH32)
Gene_590
Gene_593
Gene_594
Gene_596
Gene_601
Gene_603
Gene_705
AFMa275xb9(D12S1628)
B0768I12A2x
stSG43910
B1134M23A1y
WI15018
stsN20163
B1118L08A1x
B0675M15A2y
stsX89576
stSG30906
B0723P10A1x
stSG26056
IB2452
stSG4720
B0700H07A2x
B1134M23A1x
B0675M15A2x
stsN59820
stSG1702
AA252357
stSG31443
A008Y05
stsH94865
stSG39493
R50113
SGC30786
FB9F8
stsAA001424
1118L08
1066E19
1143P18
0742P09
1134M23
1134I23
0594P15
0932D22
0964M24
0675M15
0793B14
0627A21
RP11-0495K09
0681M13
0700H07
0786G24

FIG. 5G

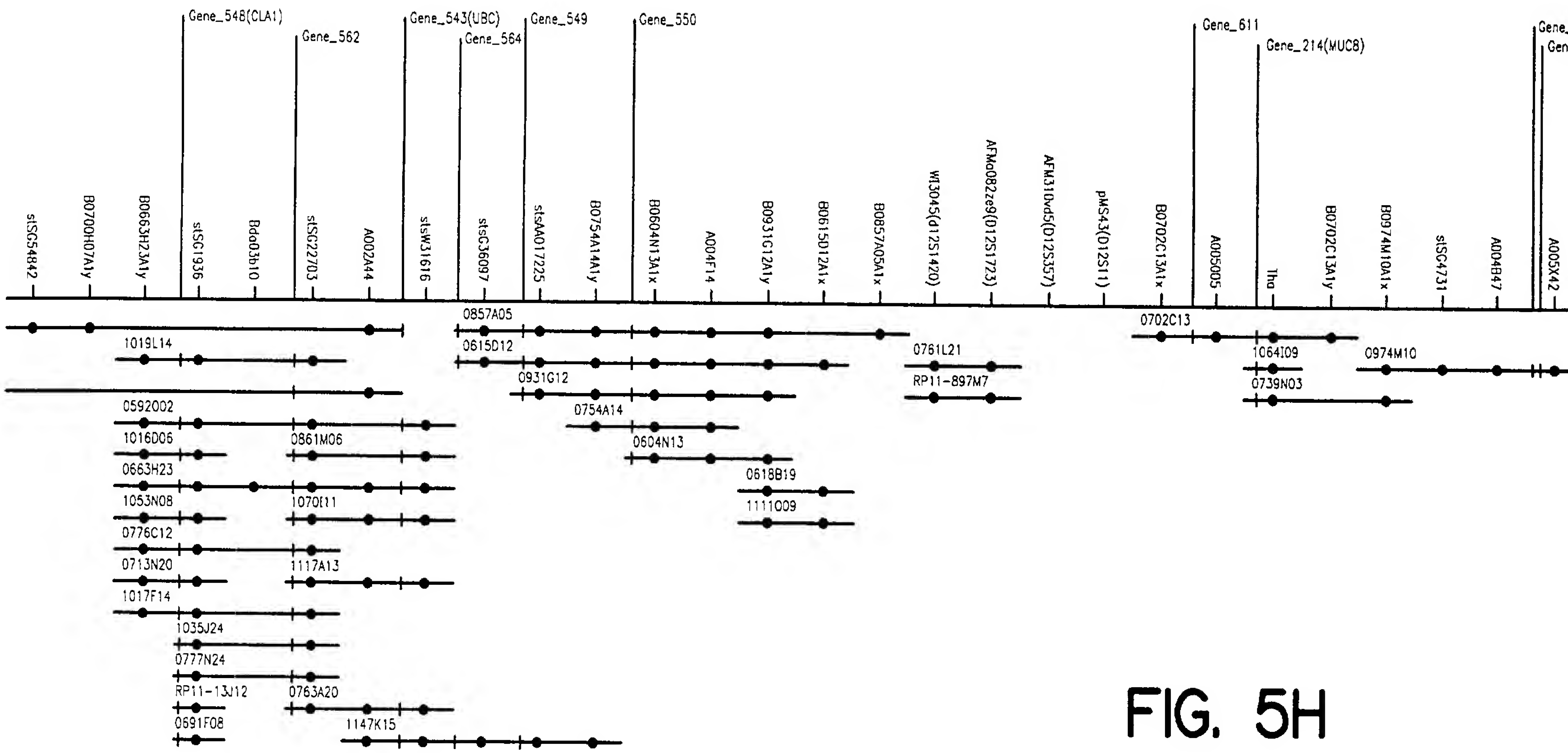
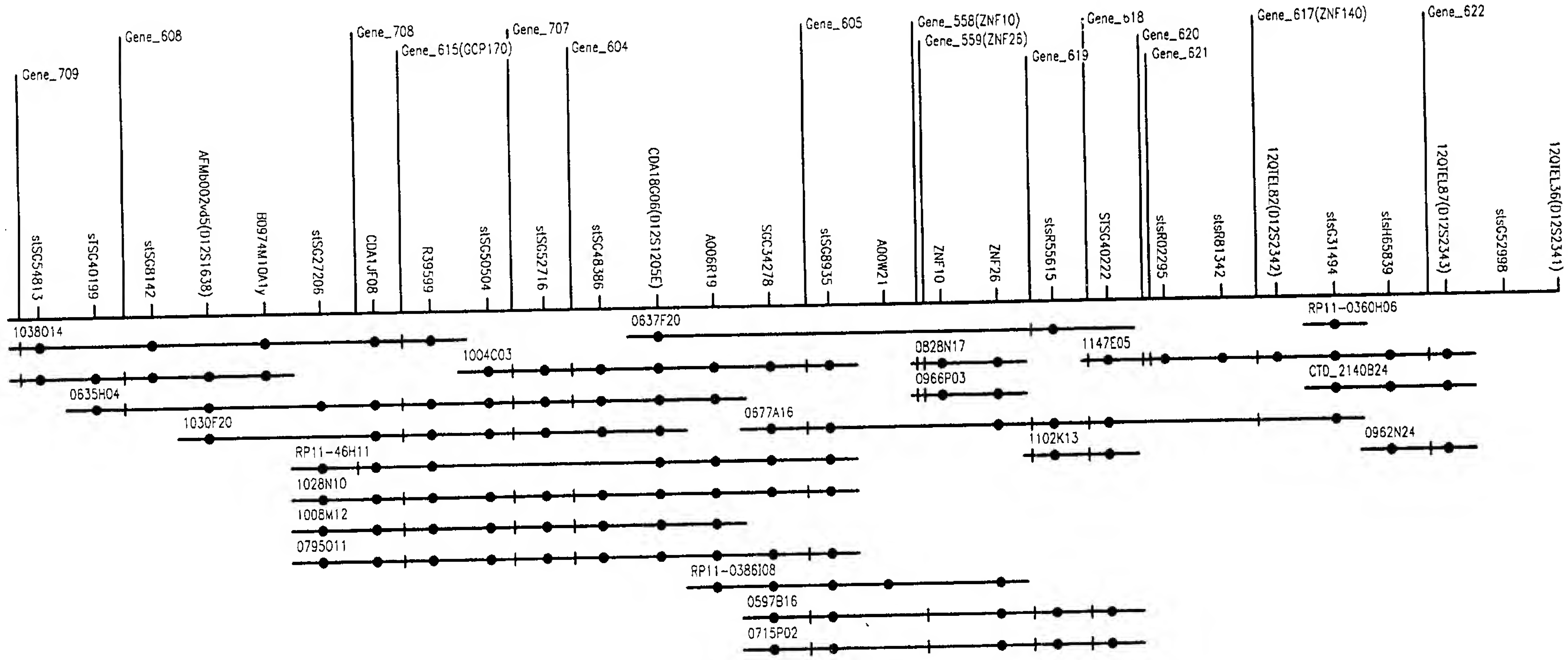

Gene_548(CLA1)
Gene_562
Gene_543(UBC)
Gene_564
Gene_549
Gene_550
Gene_611
Gene_214(MUC8)
Gene_606(POLE)
Gene_610
stSG54842
B0700H07A1y
B0663H23A1y
stSG1936
Bda03b10
stSG22703
A002A44
stsW31616
stsG36097
stsAA017225
B0754A14A1y
B0604N13A1x
A004F14
B0931G12A1y
B0615D12A1x
B0857A05A1x
WI3045(d12S1420)
AFMa082ze9(D12S1723)
AFM310vd5(D12S357)
pMS43(D12S11)
B0702C13A1x
A005005
Tha
B0702C13A1y
B0974M10A1x
stSG4731
A004B47
A005X42
1019L14
0592O02
1016D06
0663H23
1053N08
0776C12
0713N20
1017F14
1035J24
0777N24
RP11-13J12
0691F08
0861M06
1070I11
1117A13
0763A20
1147K15
0857A05
0615D12
0931G12
0754A14
0604N13
0618B19
1111O09
0761L21
RP11-897M7
0702C13
1064I09
0739N03
0974M10

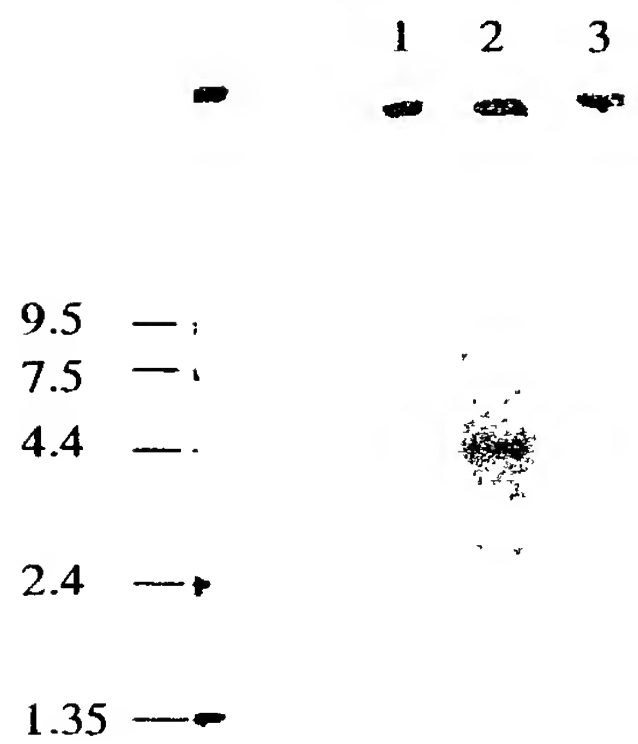
FIG. 5H



Gene_709
Gene_608
Gene_708
Gene_615(GCP170)
Gene_707
Gene_604
Gene_605
Gene_558(ZNF10)
Gene_559(ZNF26)
Gene_619
Gene_618
Gene_620
Gene_621
Gene_617(ZNF140)
Gene_622
stSG54813
sTSG40199
stSG8142
AFMb002vd5(D12S1638)
B0974M10A1y
stSG27206
CDA1JF08
R39599
stSG50504
stSG52716
stSG48386
CDA18G06(D12S1205E)
A006R19
SGC34278
stSG8935
A00W21
ZNF10
ZNF26
stsR55615
STSG40222
stsR02295
stsR81342
12QTEL82(D12S2342)
stsG31494
stsH65839
12QTEL87(D12S2343)
stsG52998
12QTEL36(D12S2341)
1038O14
0635H04
1030F20
1004C03
RP11-46H11
1028N10
1008M12
0795O11
0637F20
0677A16
RP11-0386I08
0597B16
0715P02
0828N17
0966P03
1147E05
1102K13
RP11-0360H06
CTD_2140B24
0962N24

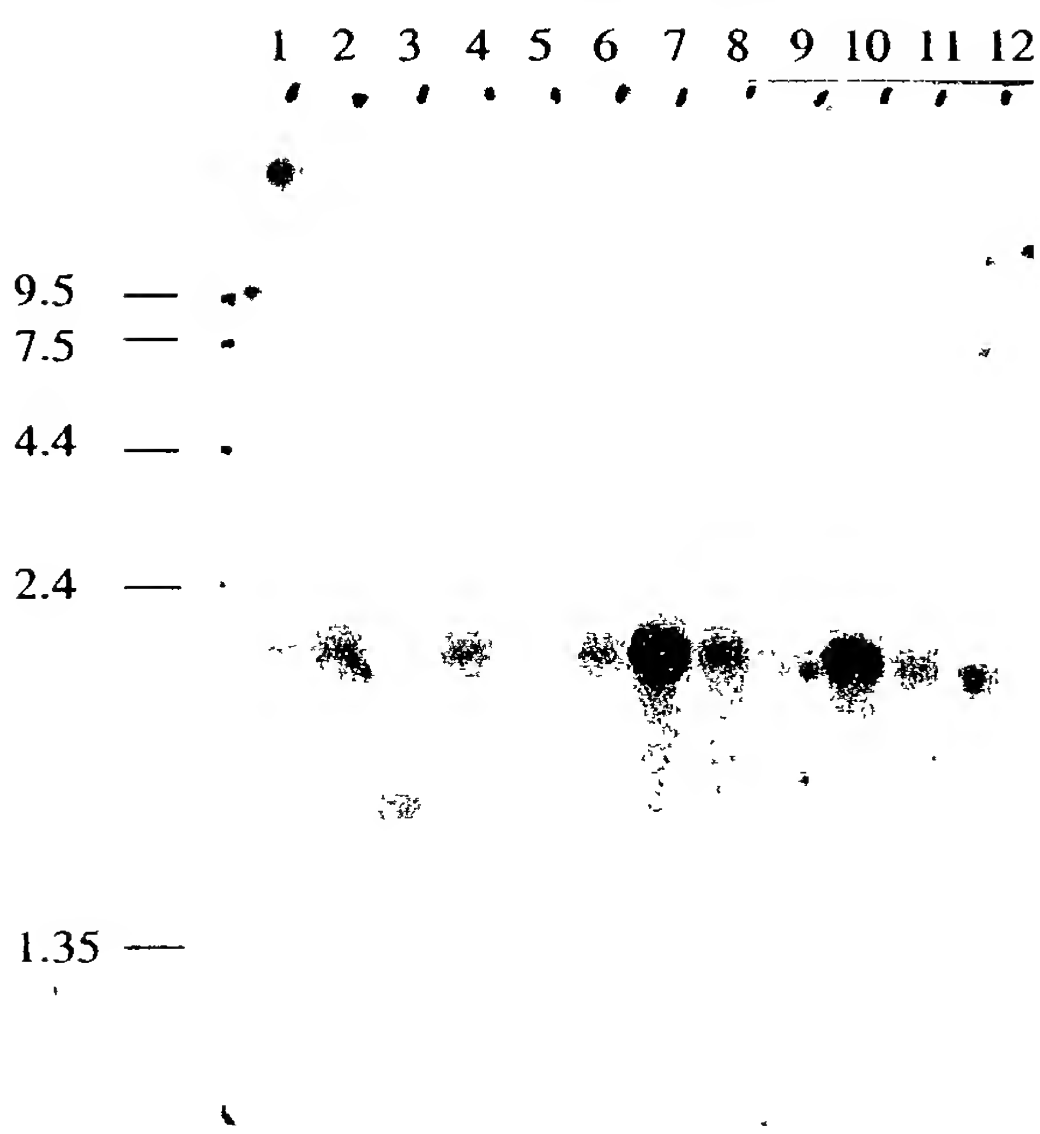
FIG. 5I

Gene 214



1. Lymphoblastoid cell line
2. Lung
3. Trachea

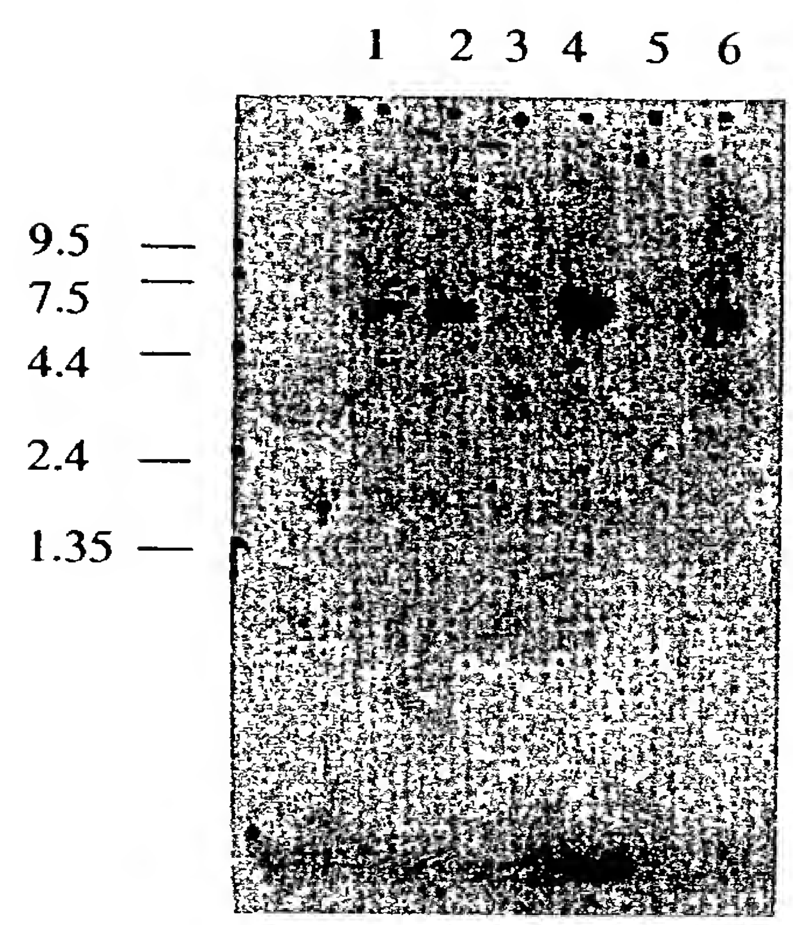
Gene 436



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

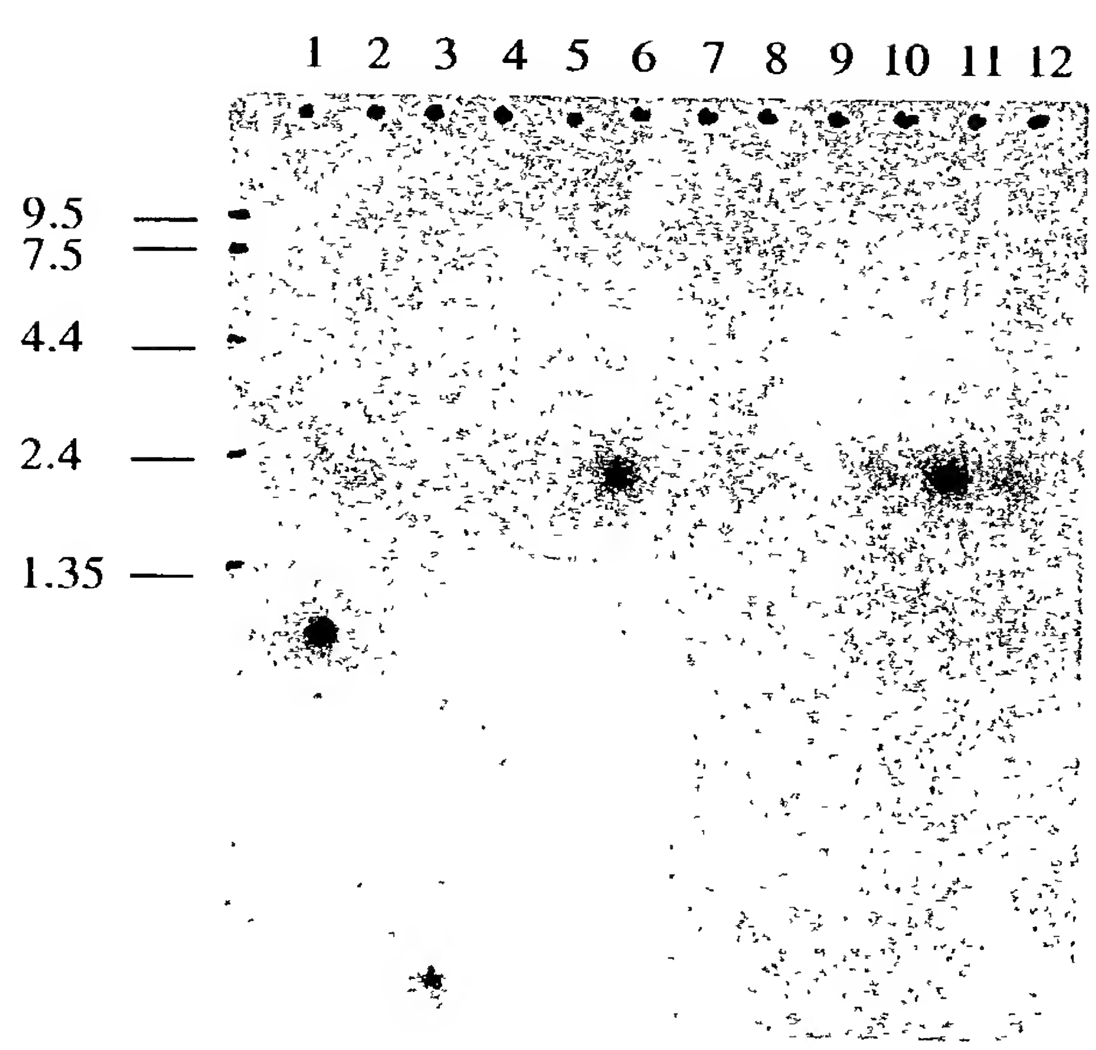
FIG. 6A

Gene 454



1. Spleen
2. Lymph
3. Thymus
4. Leukocytes
5. Bone Marrow
6. Fetal Liver

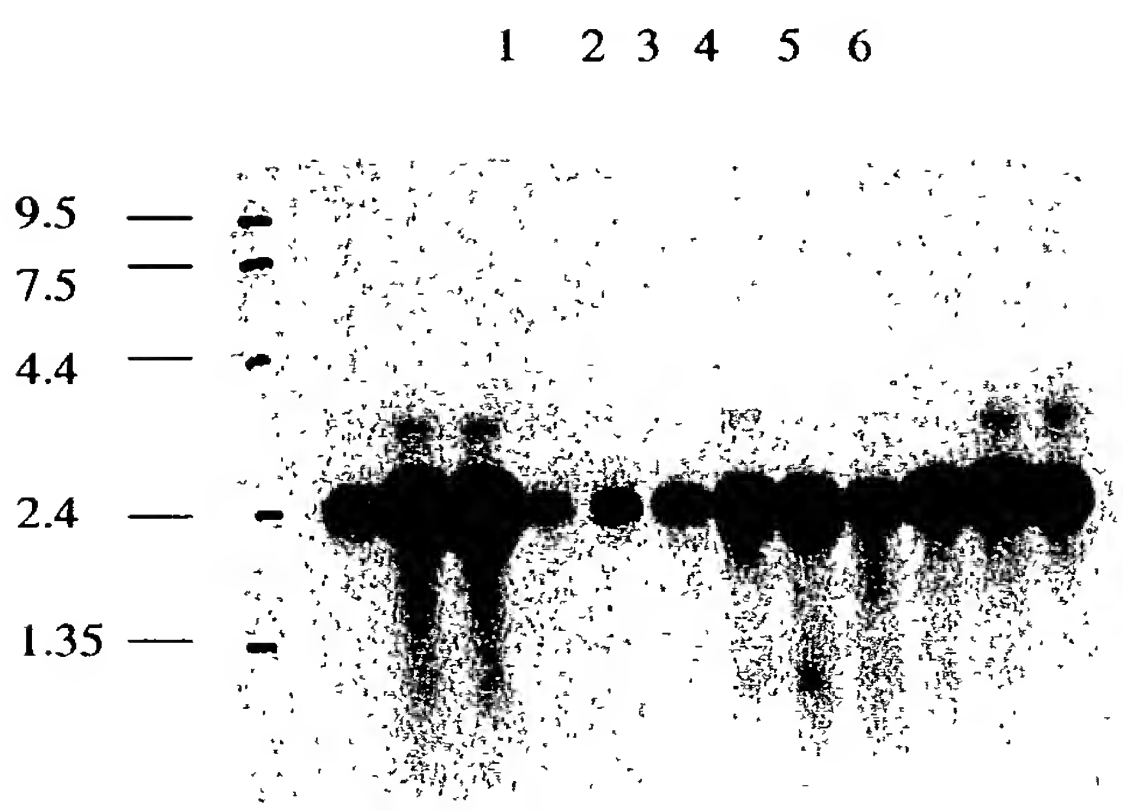
Gene 515



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

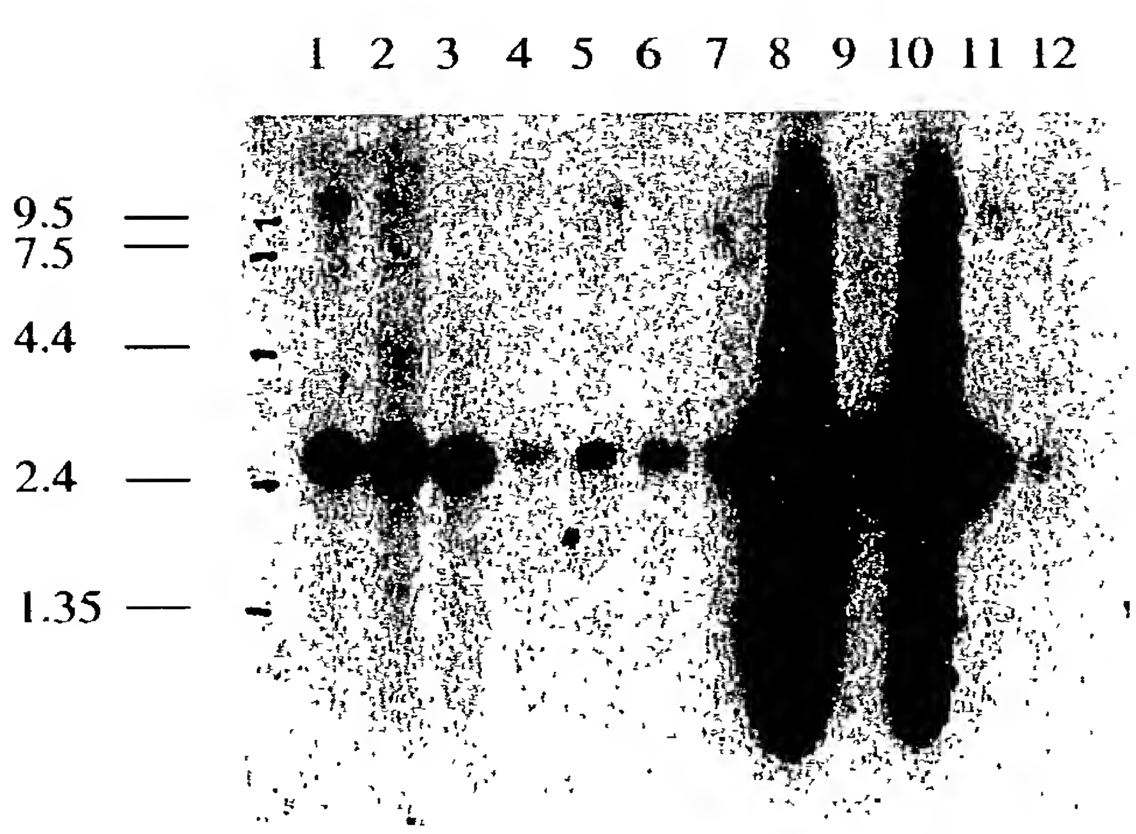
FIG. 6B

Gene 543



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

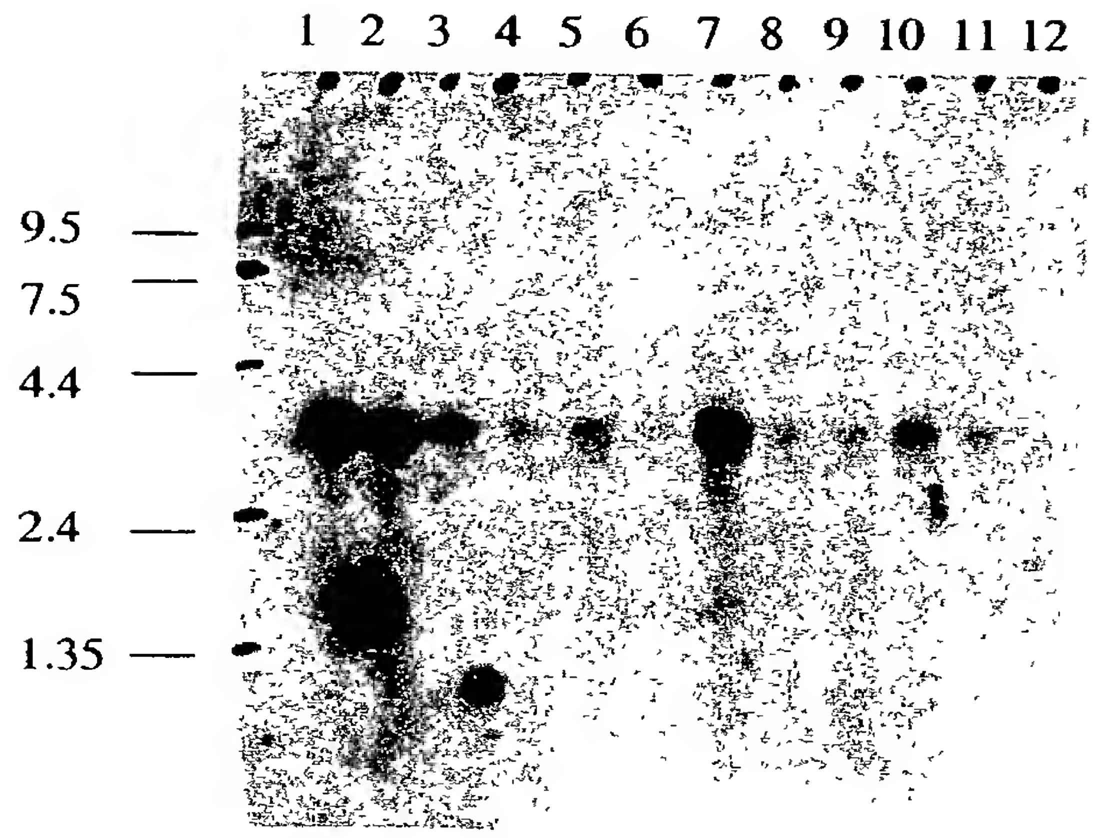
Gene 548



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

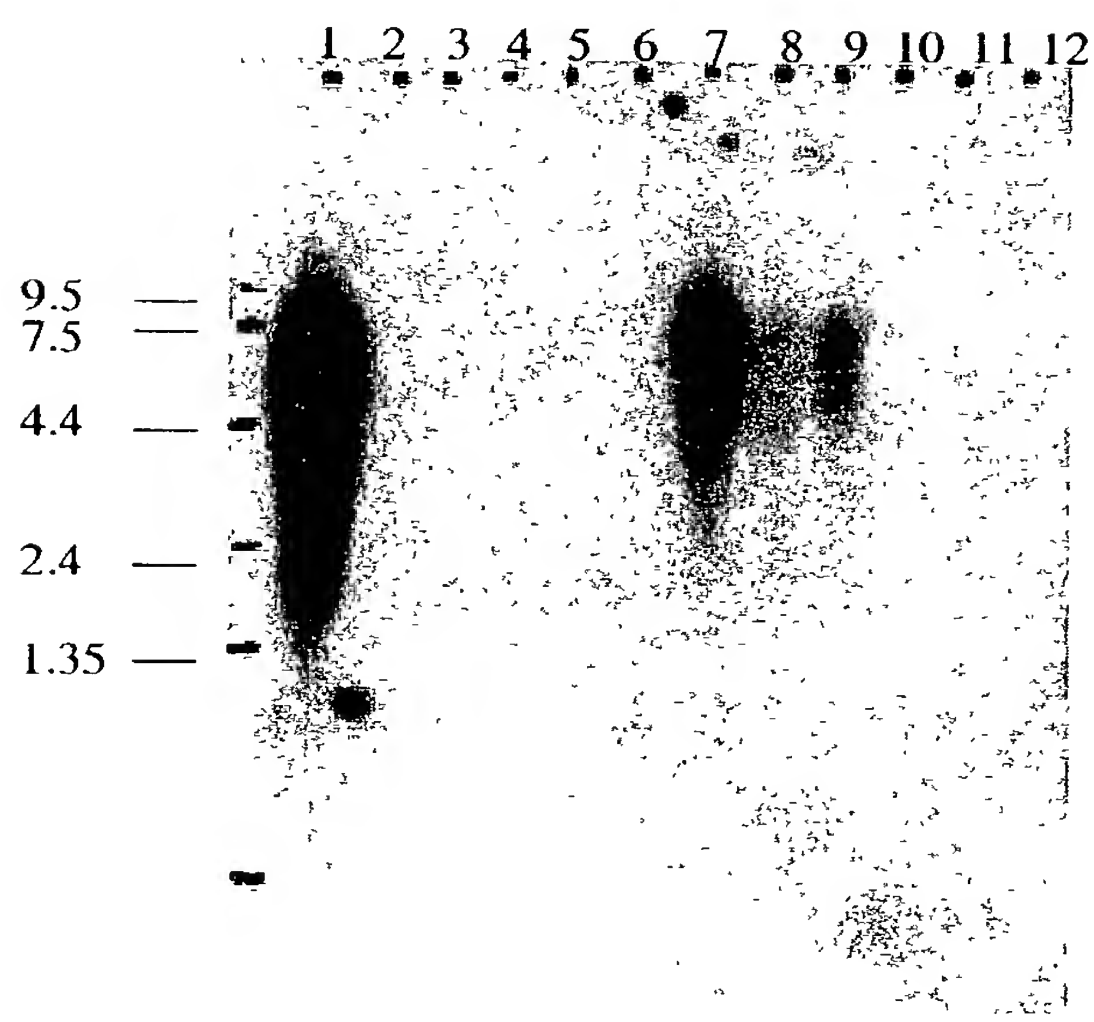
FIG. 6C

Gene 550



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

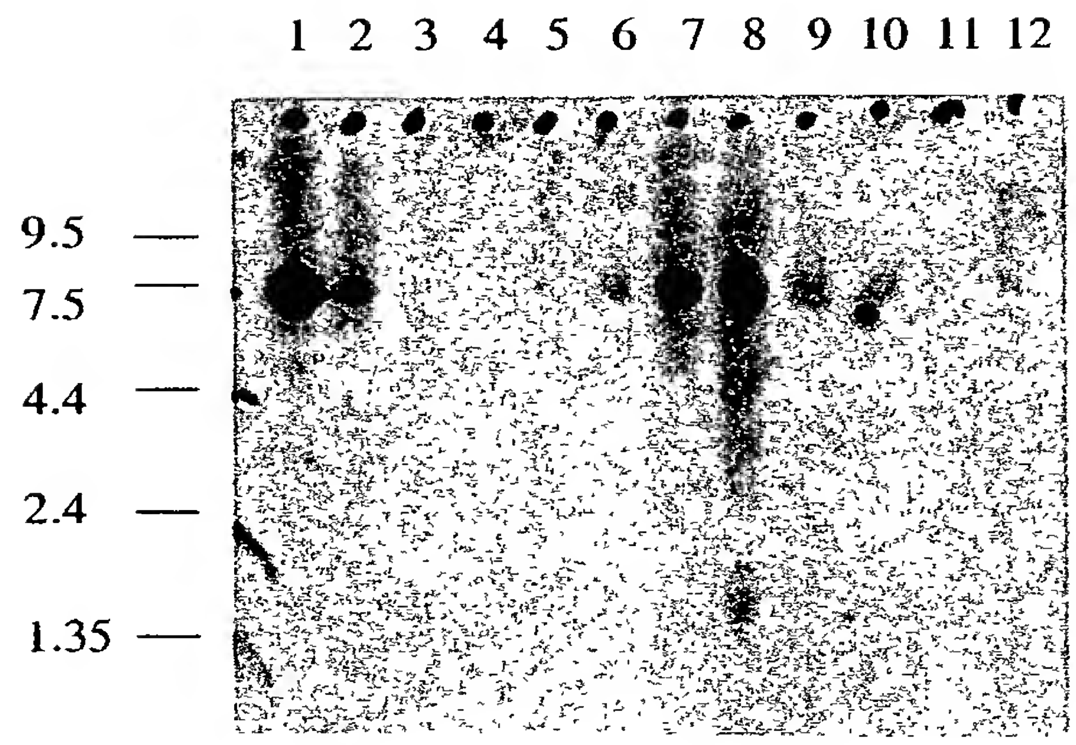
Gene 561



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

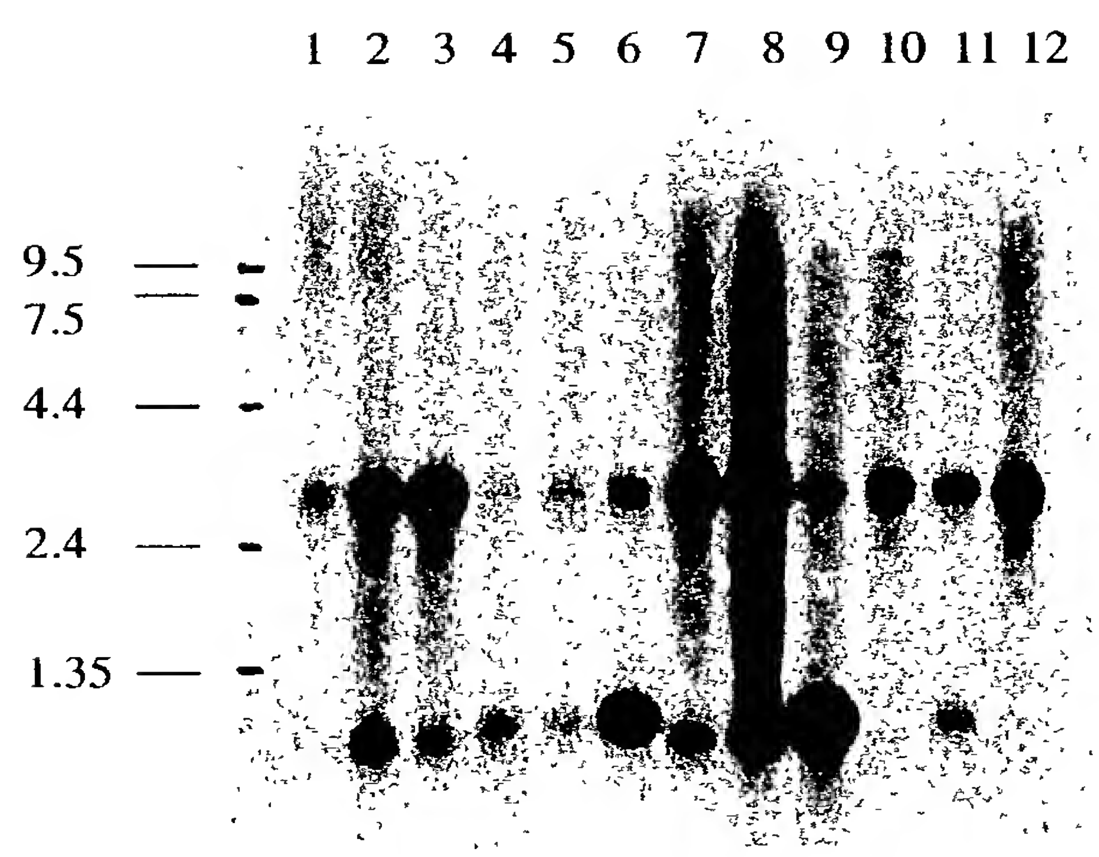
FIG. 6D

Gene 564



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

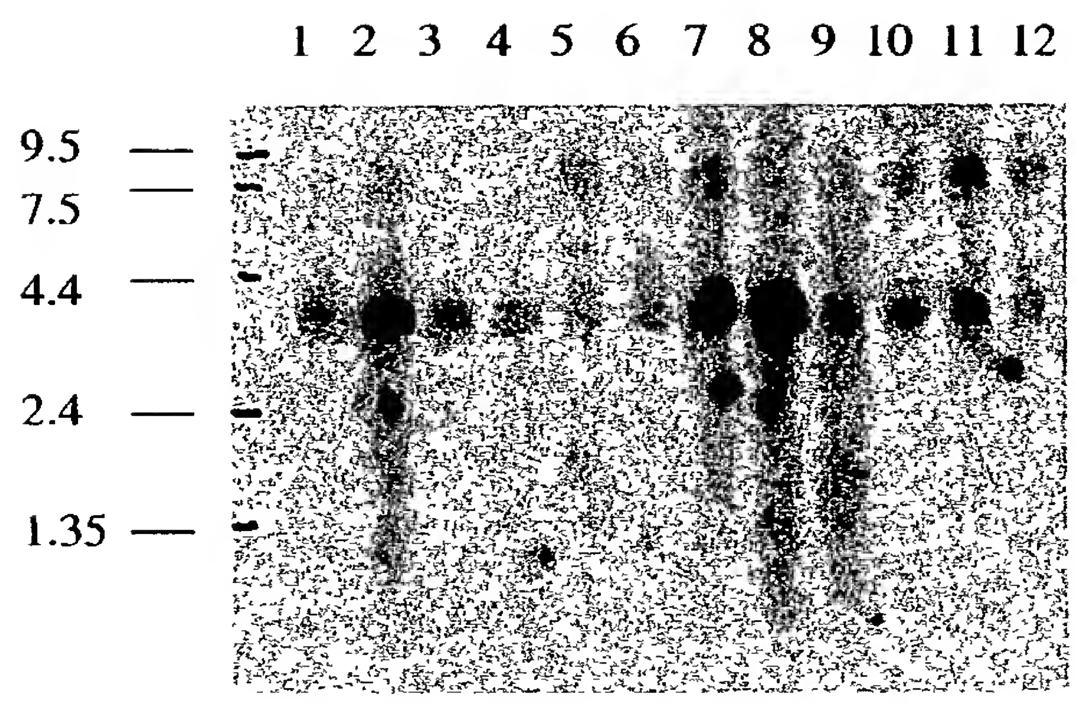
Gene 570



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

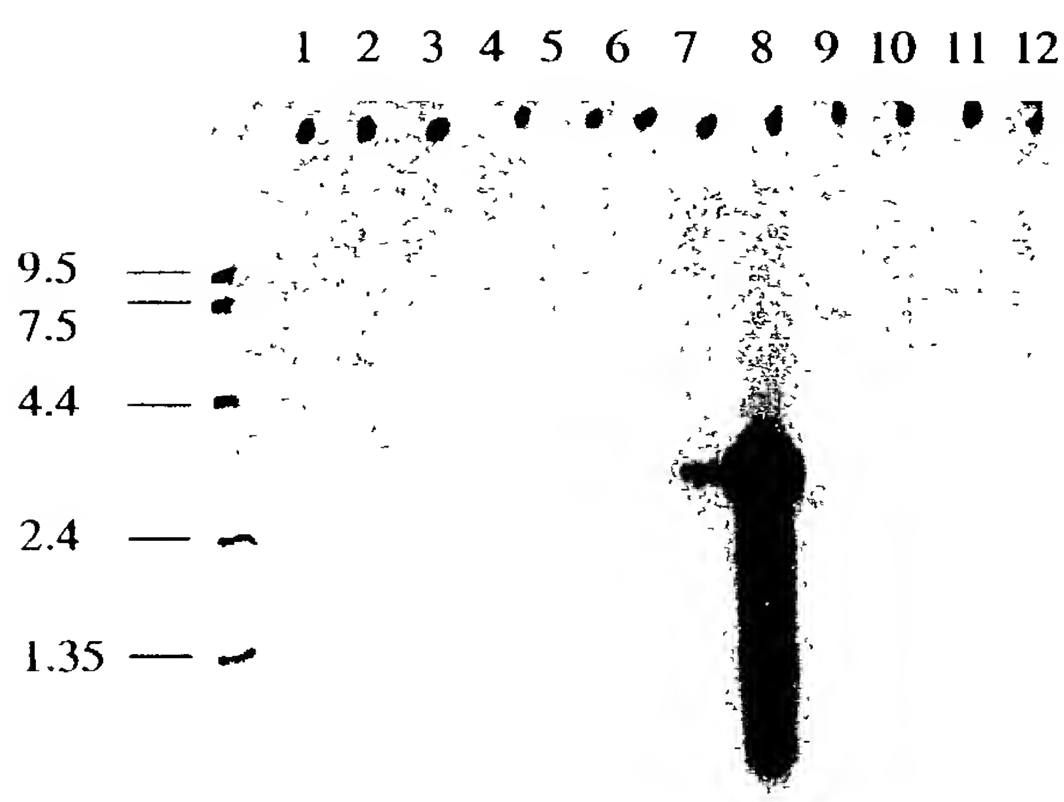
FIG. 6E

Gene 576



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

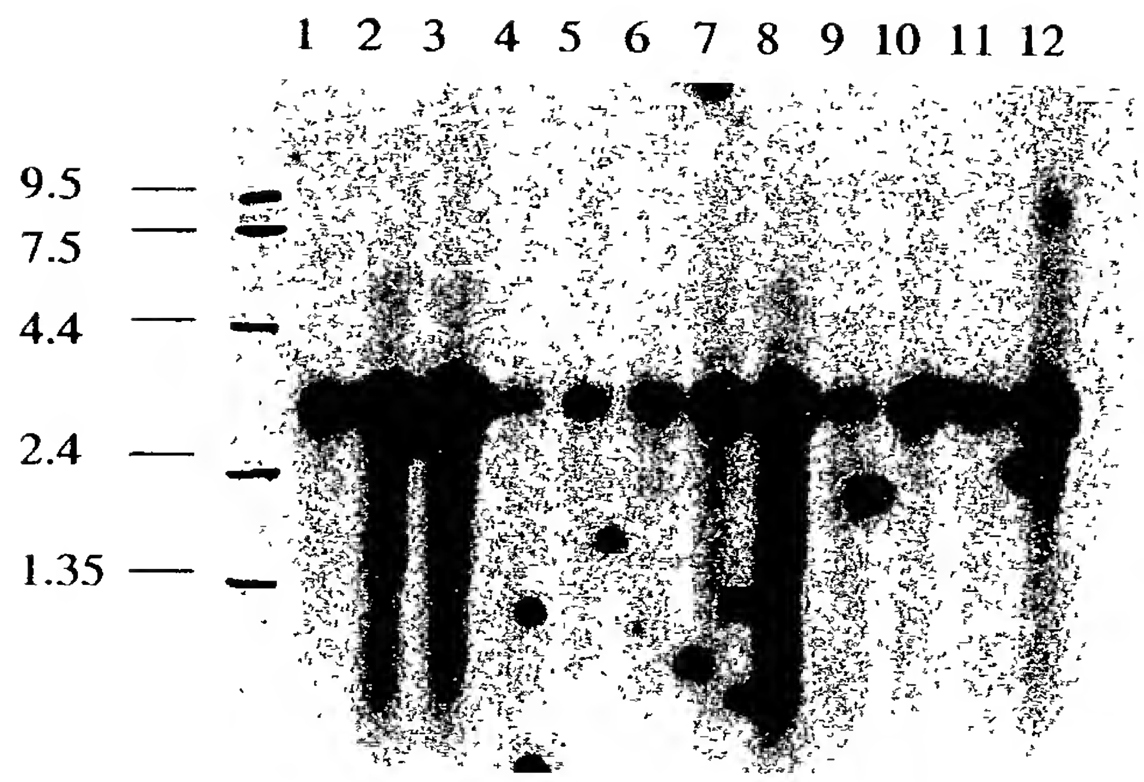
Gene 577



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

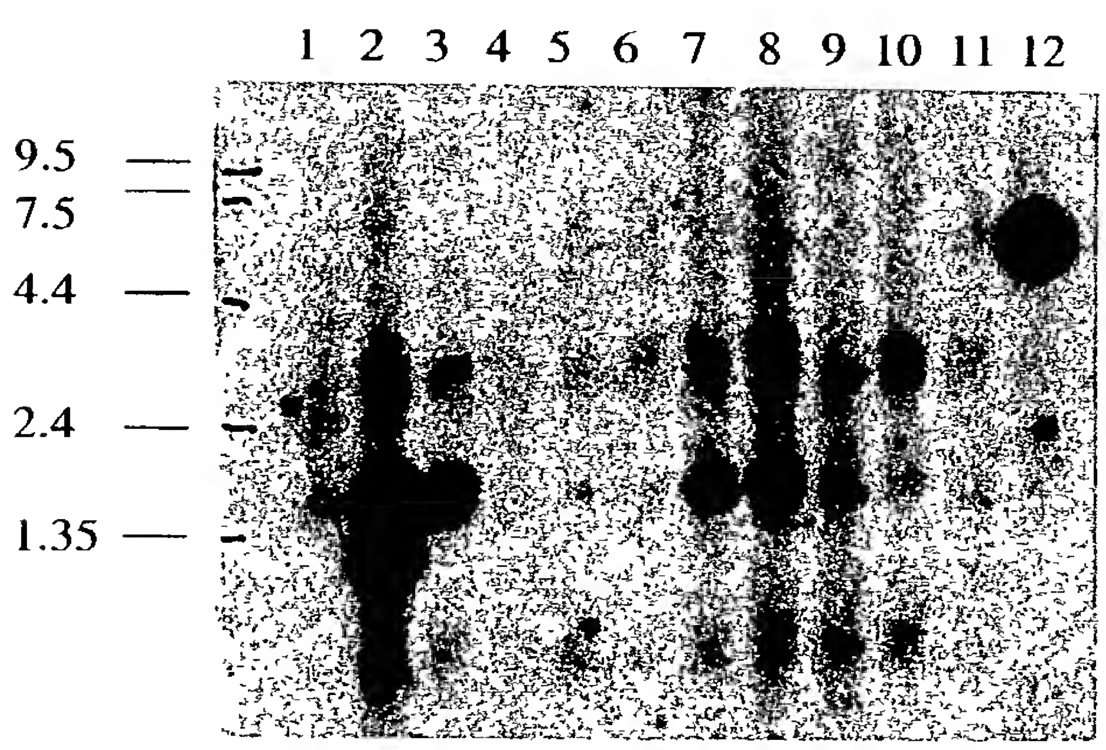
FIG. 6F

Gene 578



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

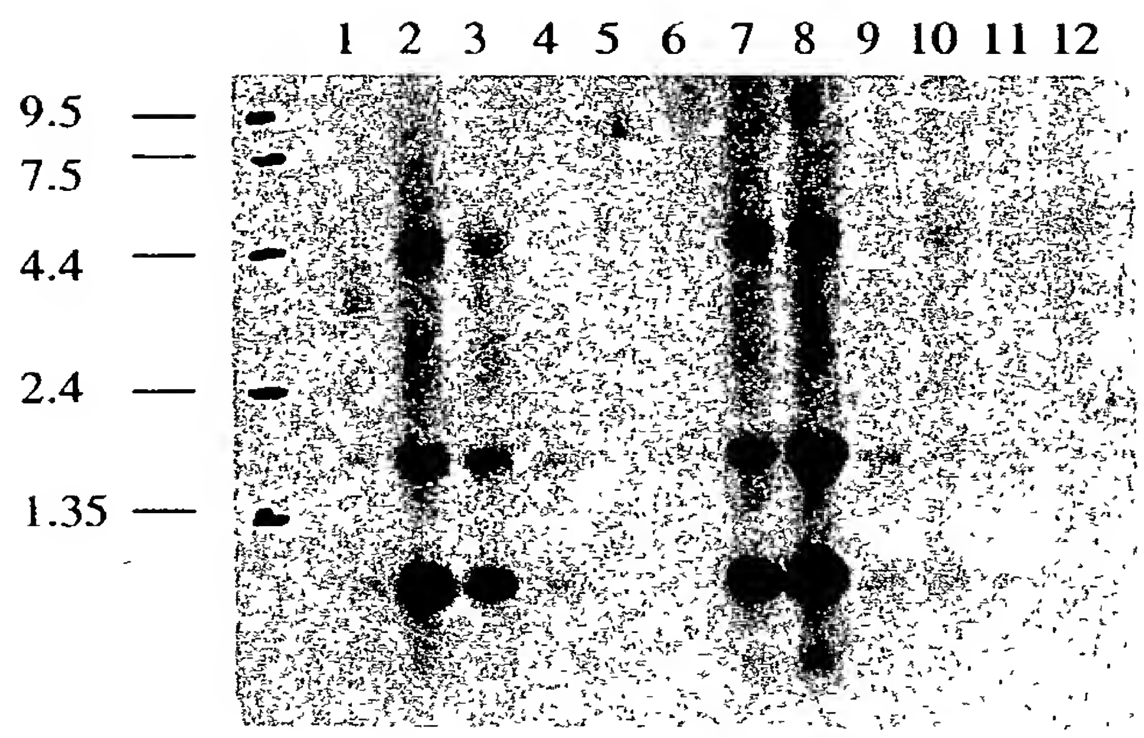
Gene 579



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

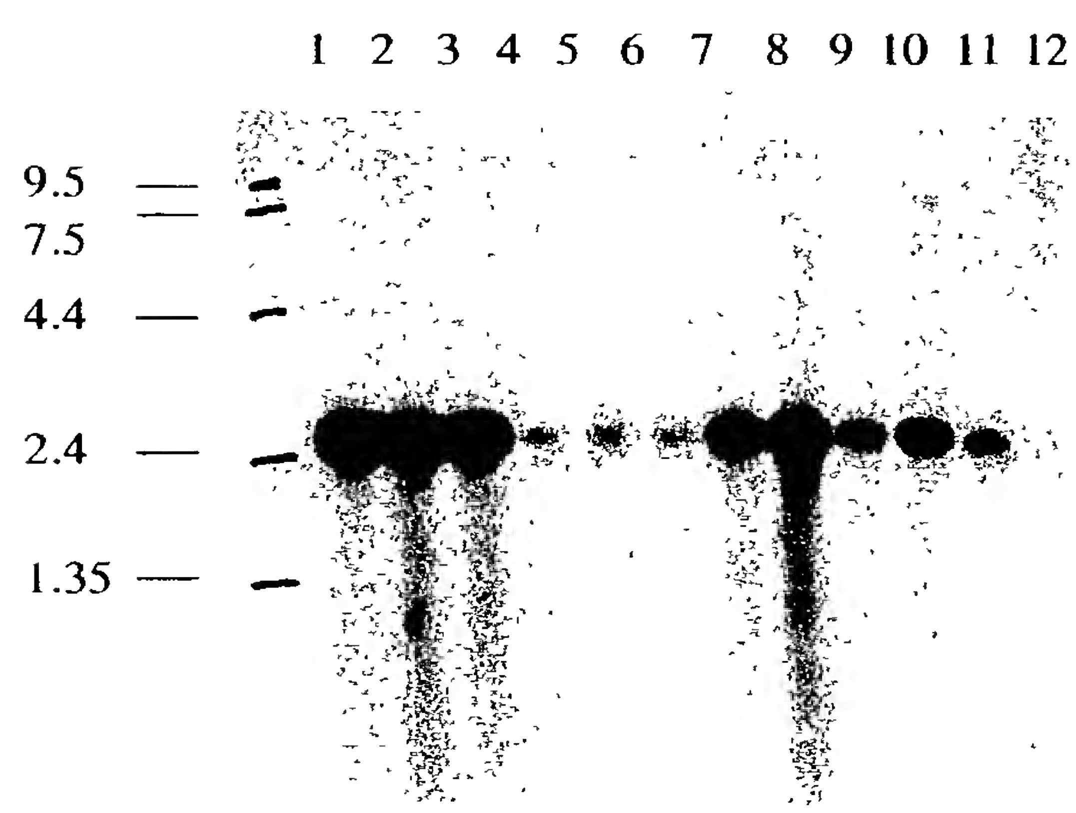
FIG. 6G

Gene 580



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

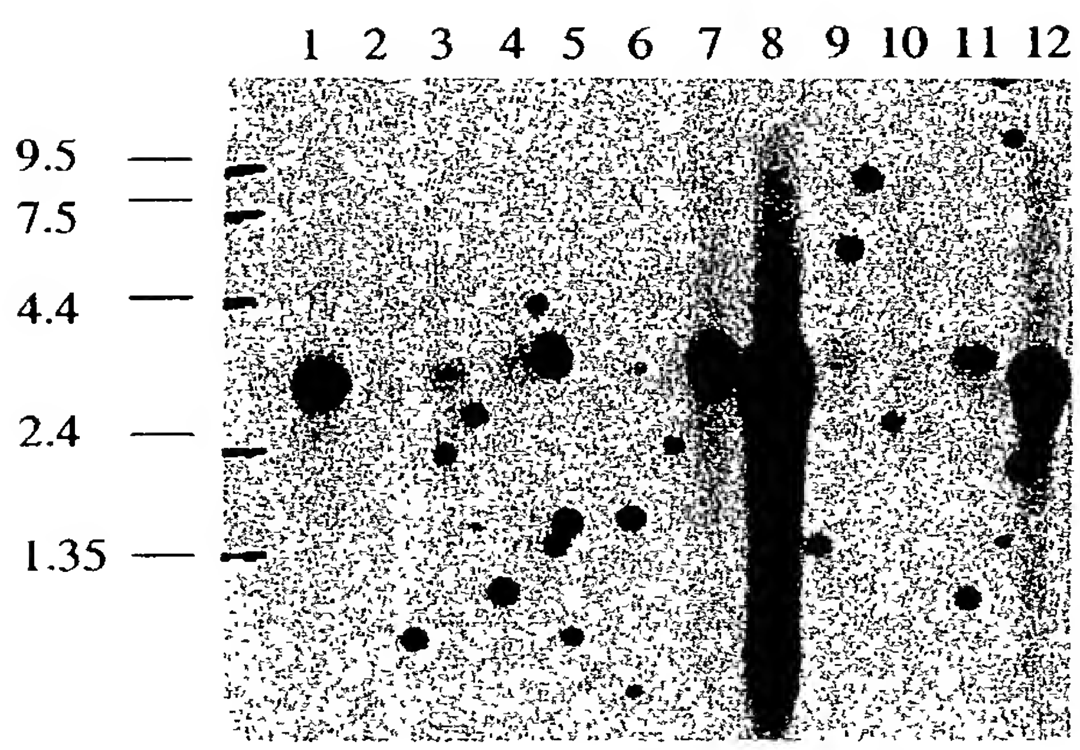
Gene 581



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

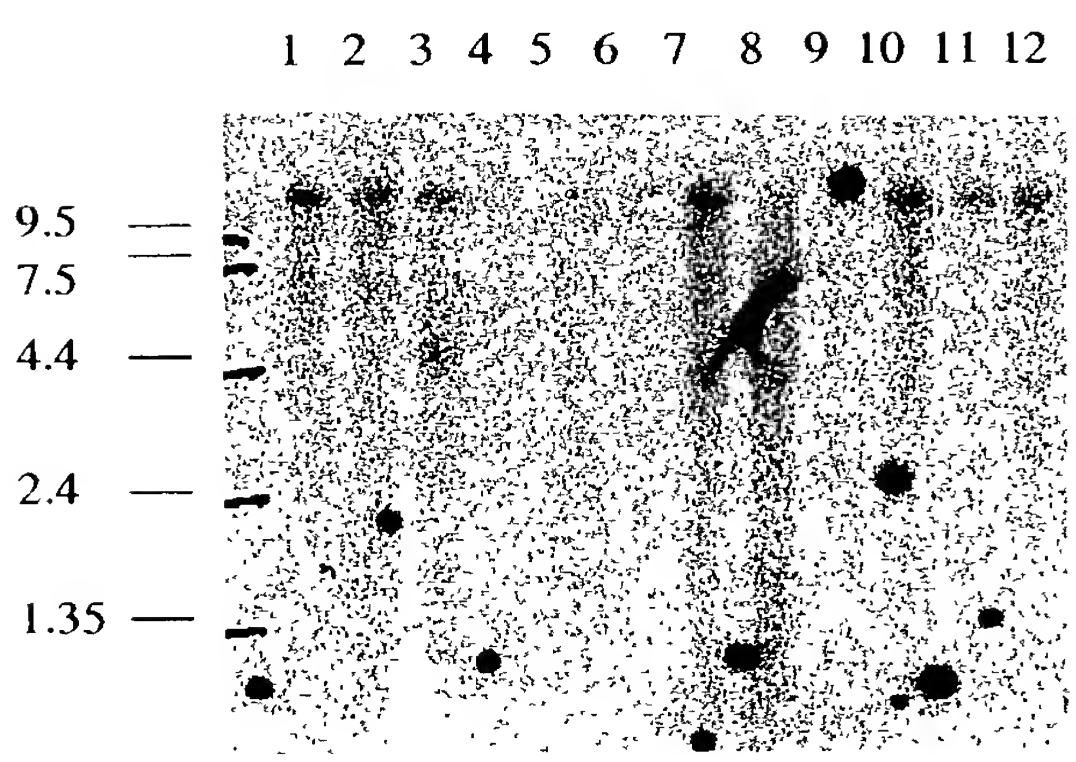
FIG. 6H

Gene 583



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

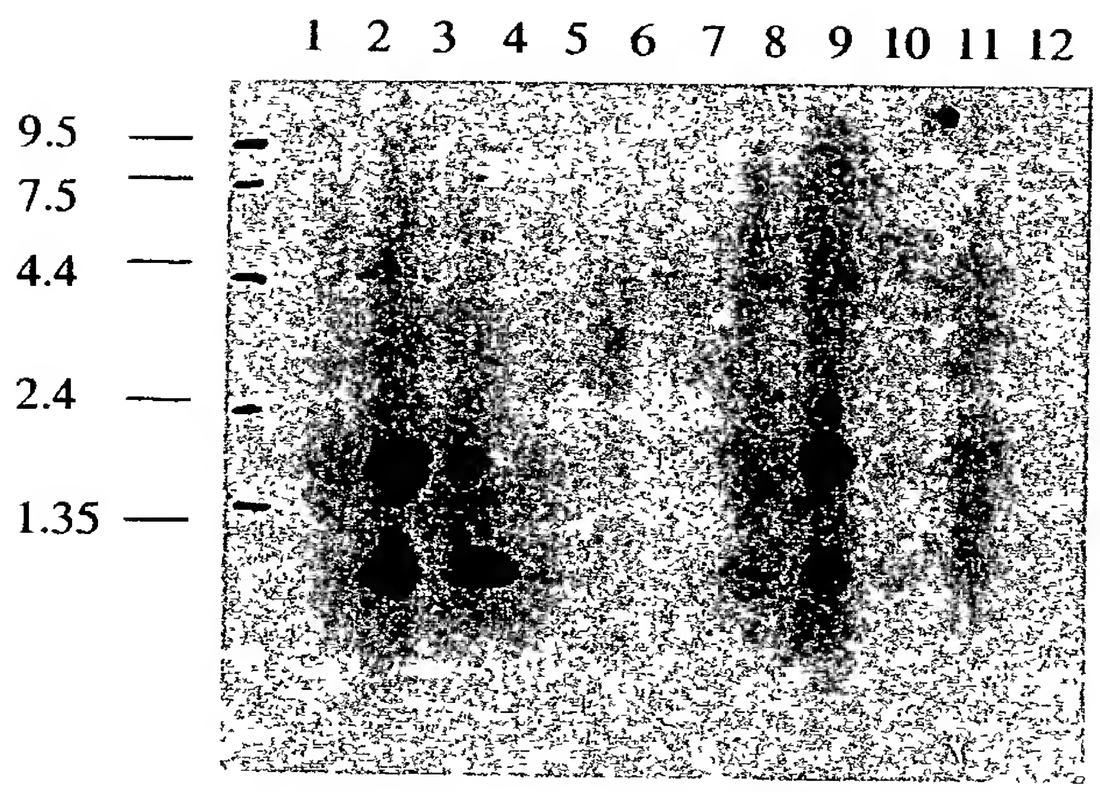
Gene 589



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

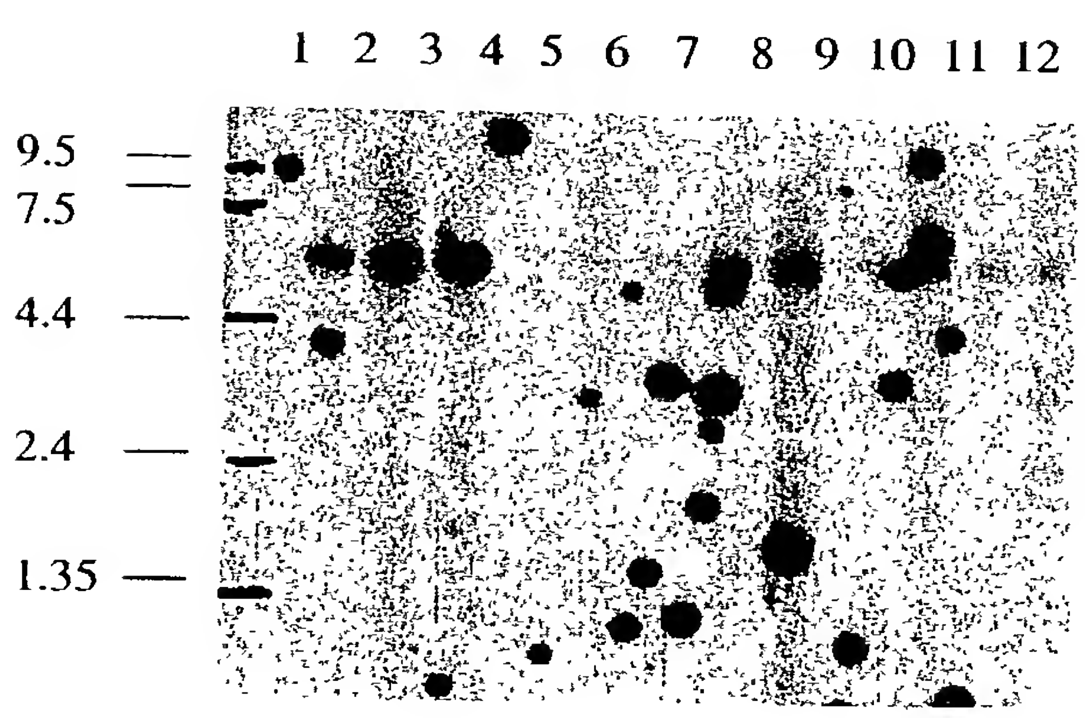
FIG. 6I

Gene 590



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

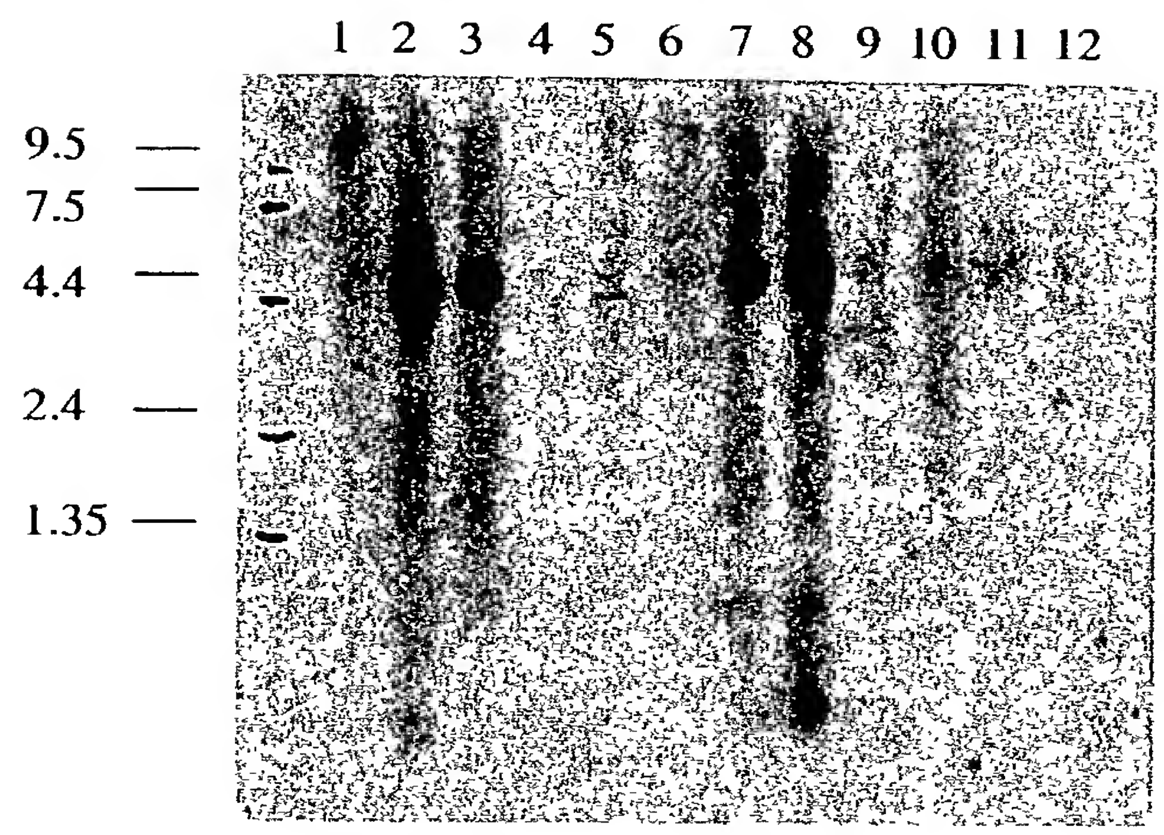
Gene 592



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

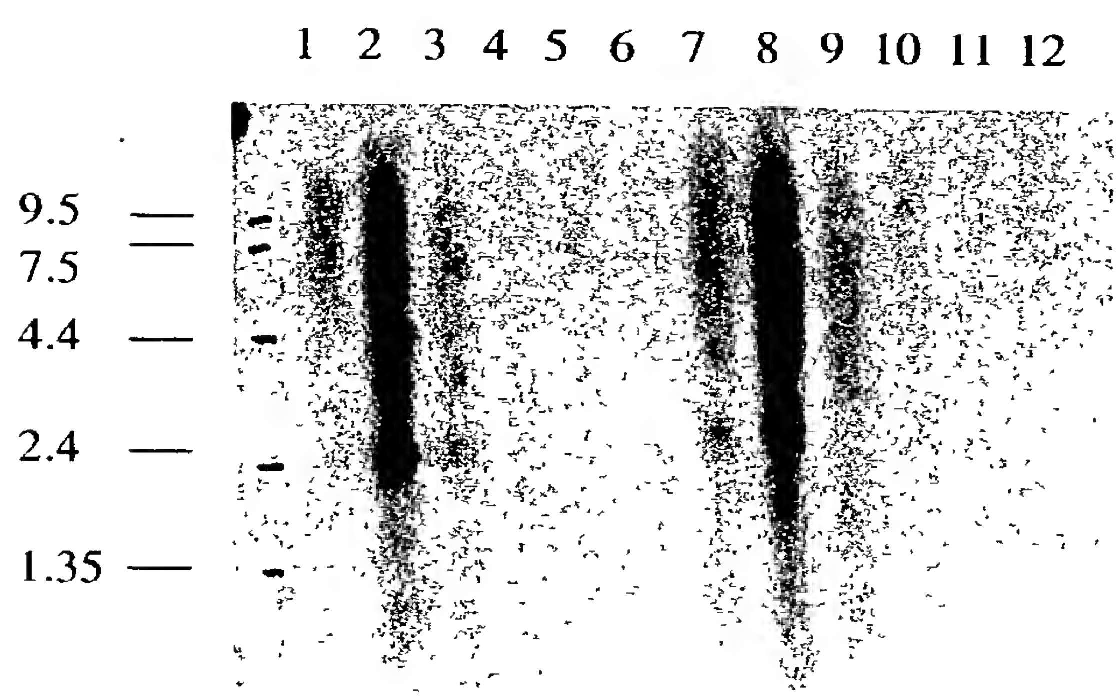
FIG. 6J

Gene 594



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

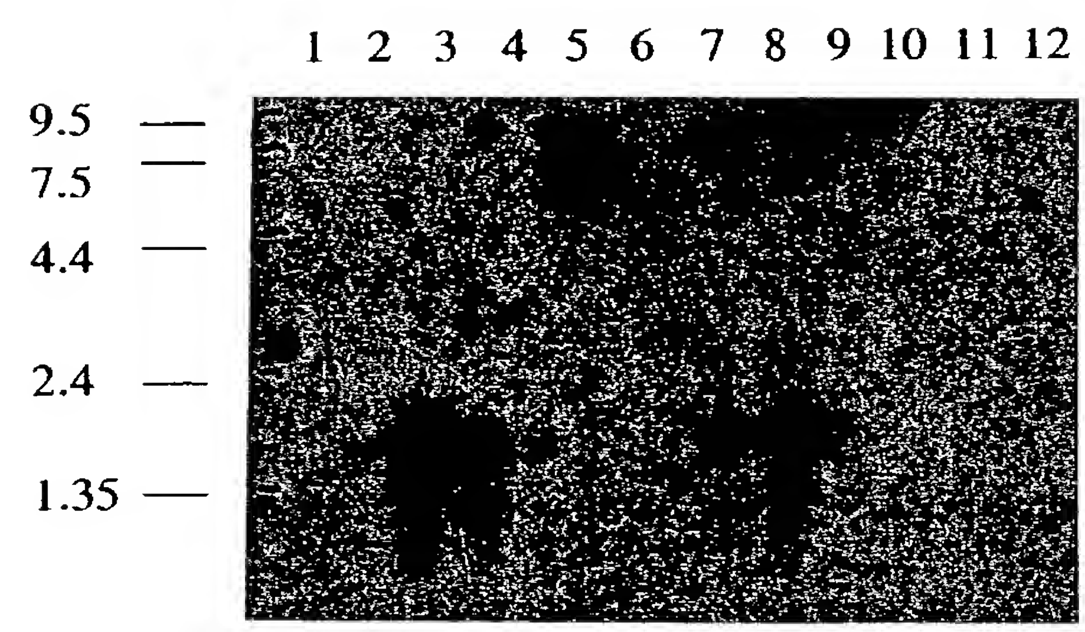
Gene 595



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

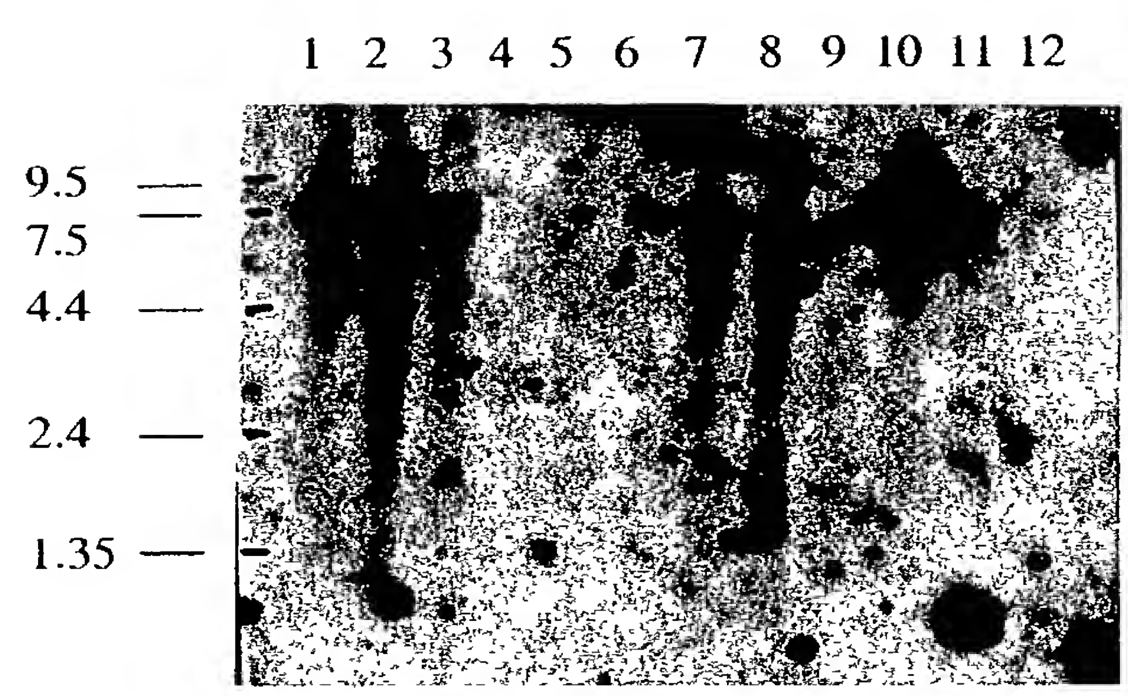
FIG. 6K

Gene 596



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

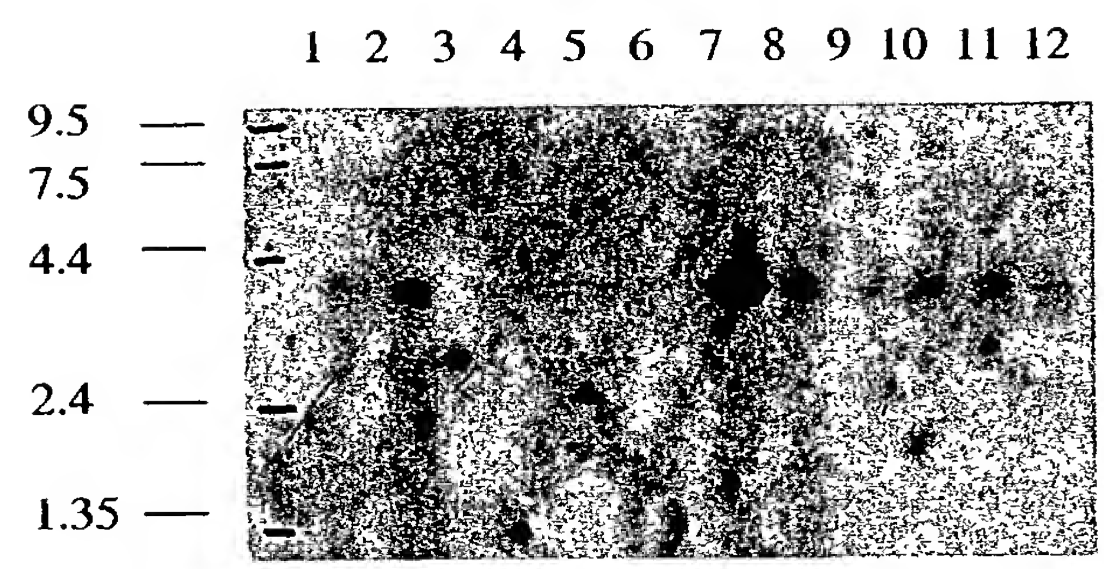
Gene 604



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

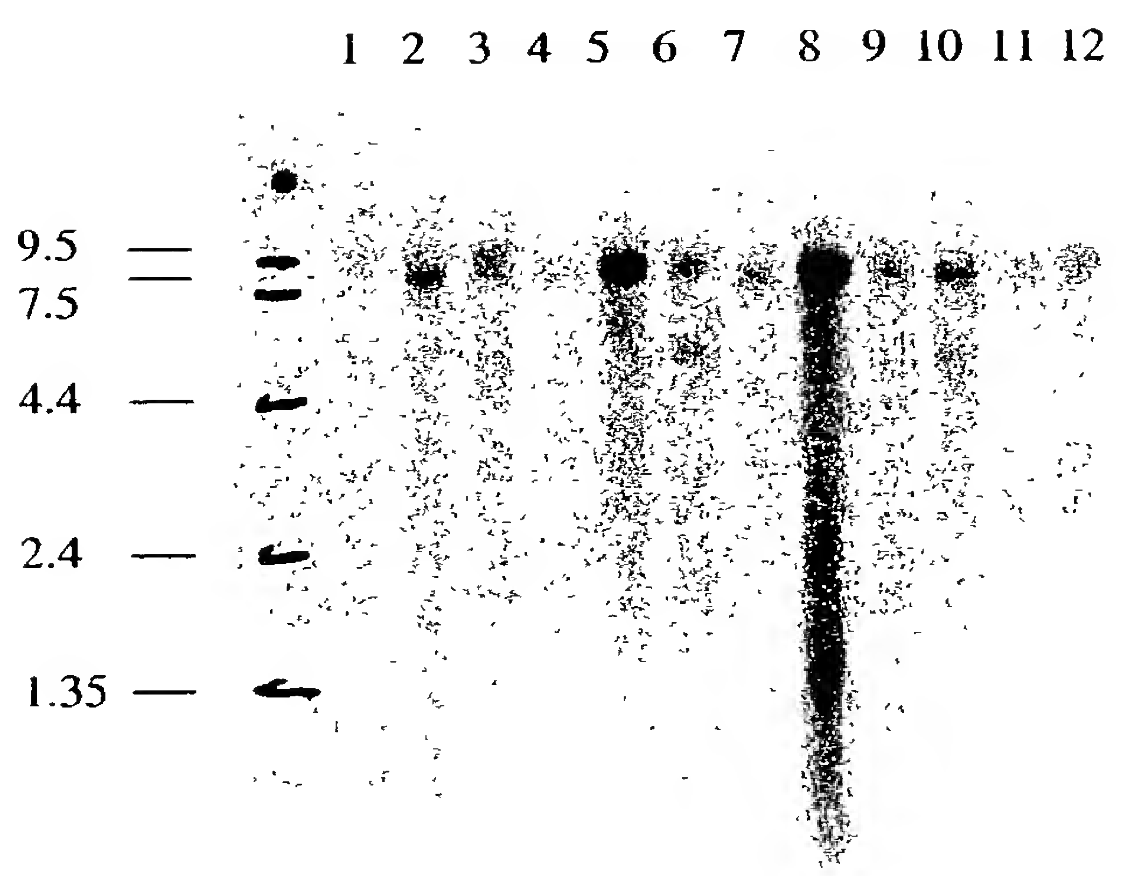
FIG. 6L

Gene 605



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

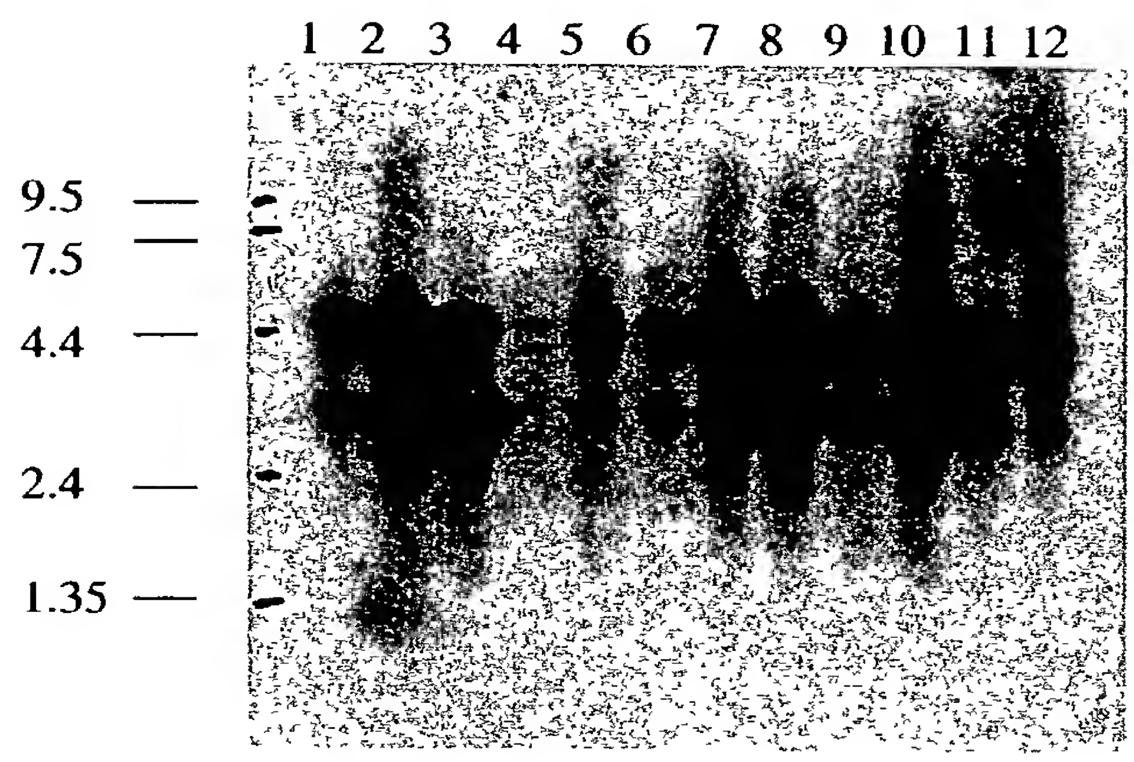
Gene 606



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

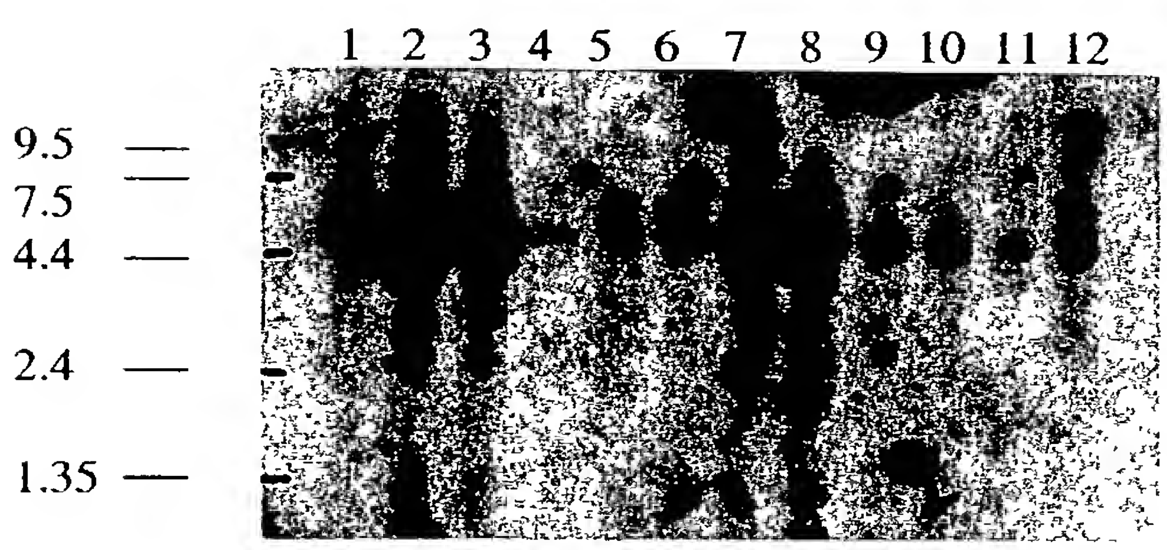
FIG. 6M

Gene 608



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

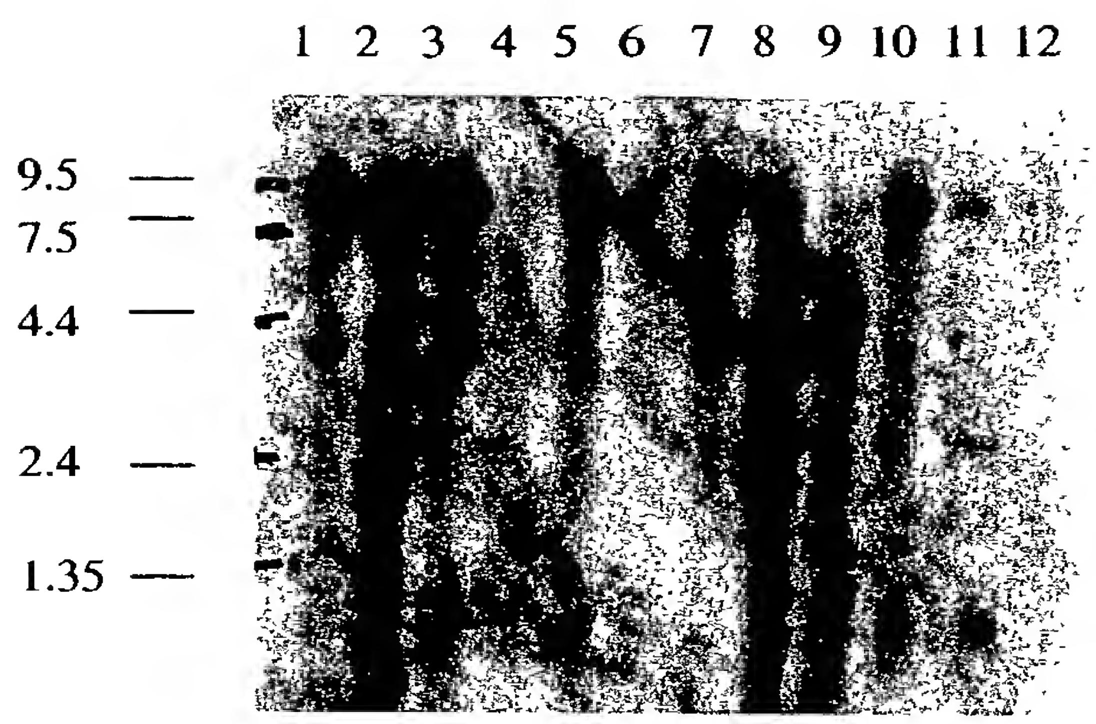
Gene 611



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

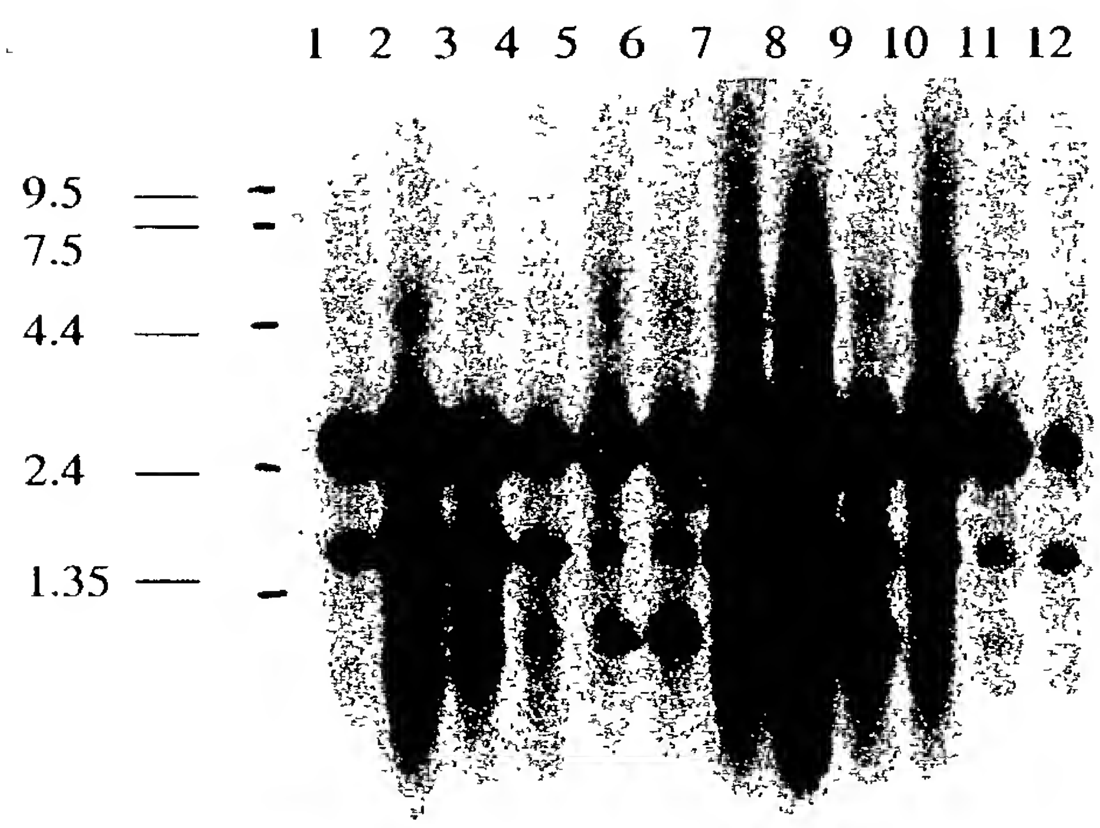
FIG. 6N

Gene 615



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

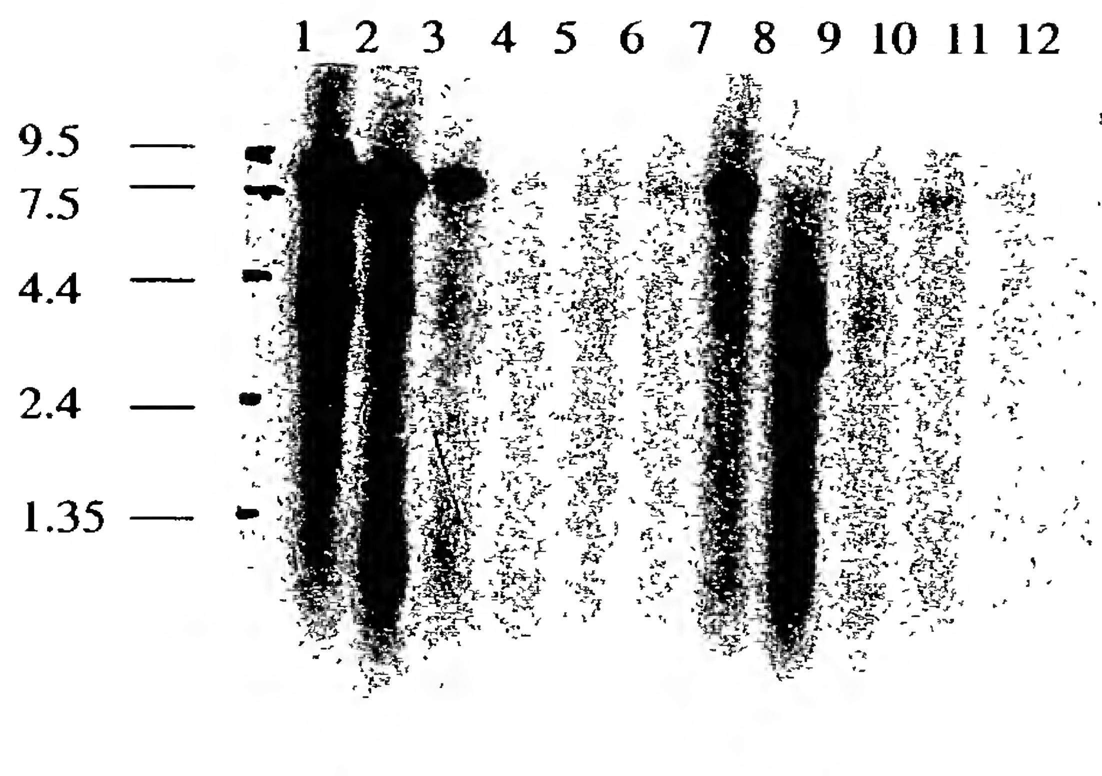
Gene 617



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

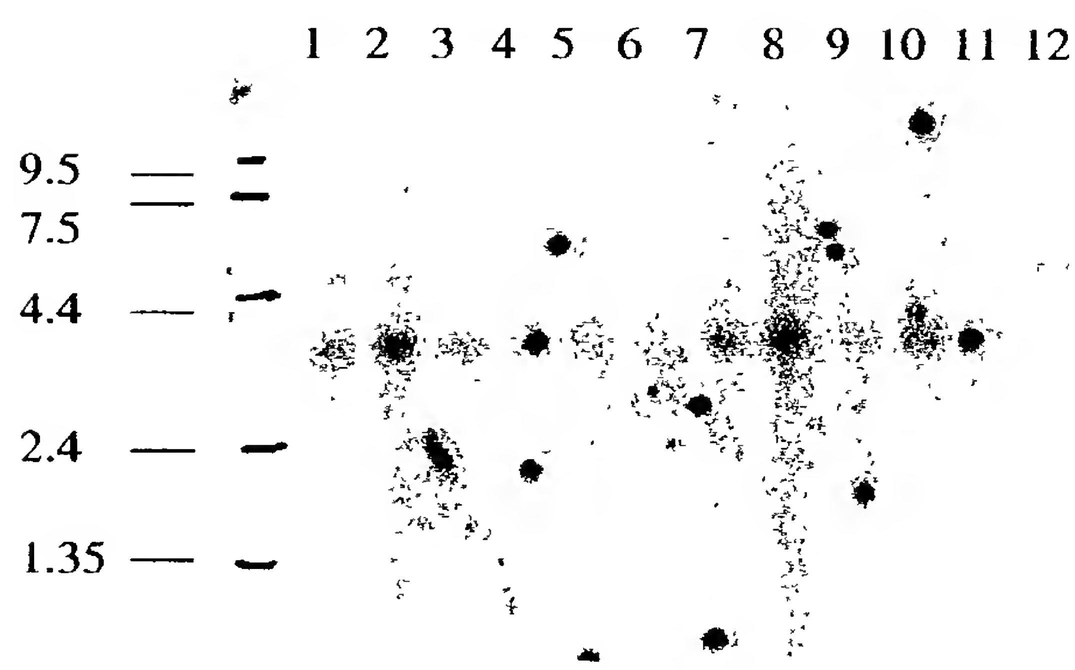
FIG. 6O

Gene 618



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

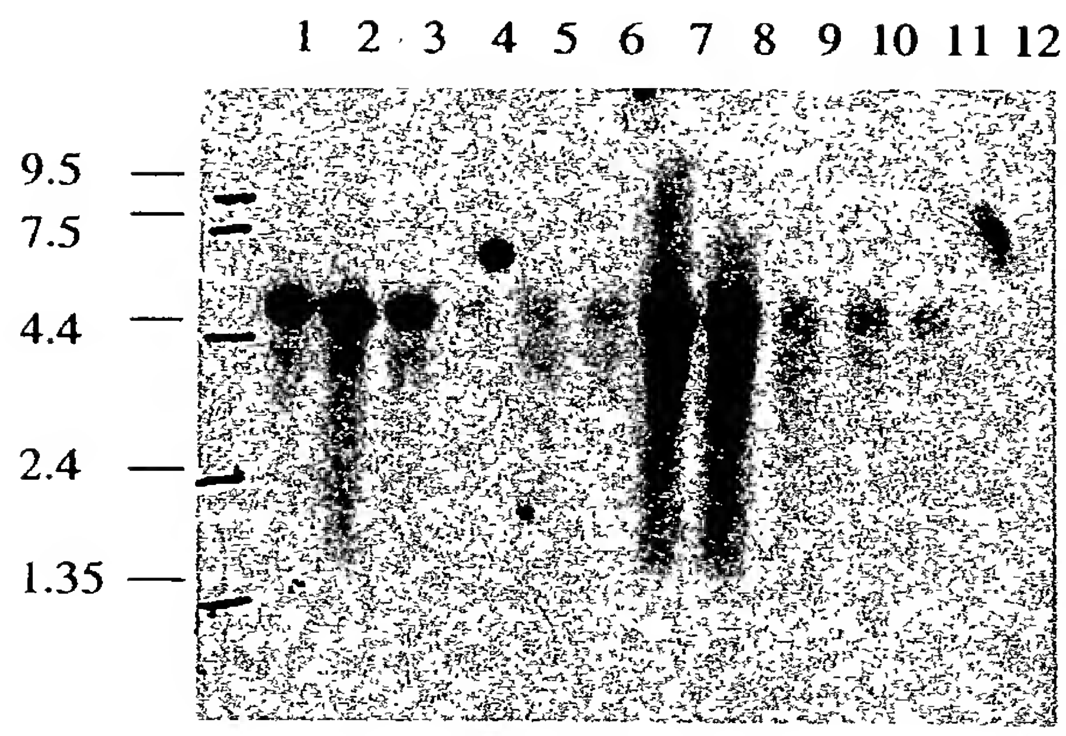
Gene 619



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

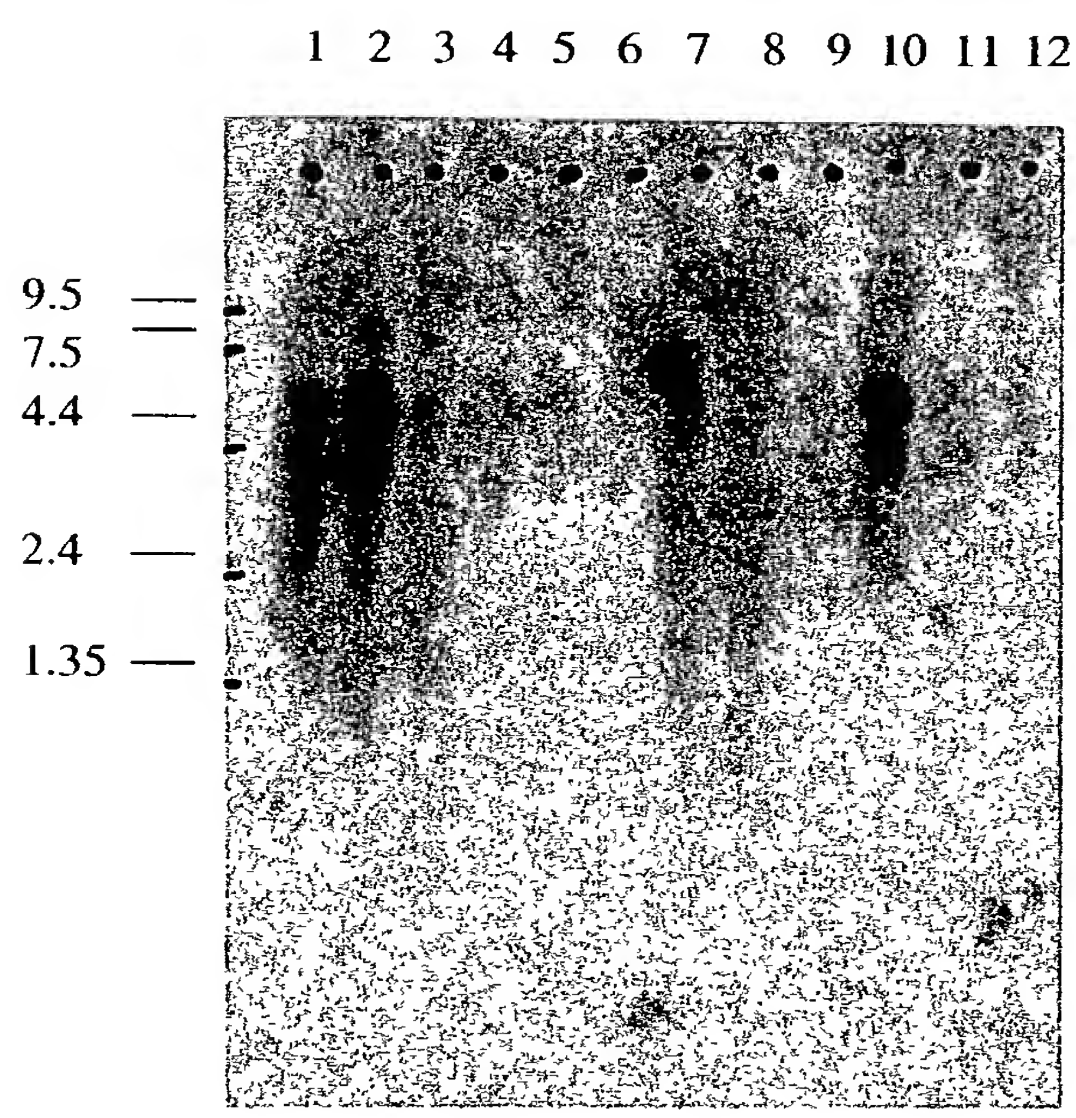
FIG. 6P

Gene 621



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

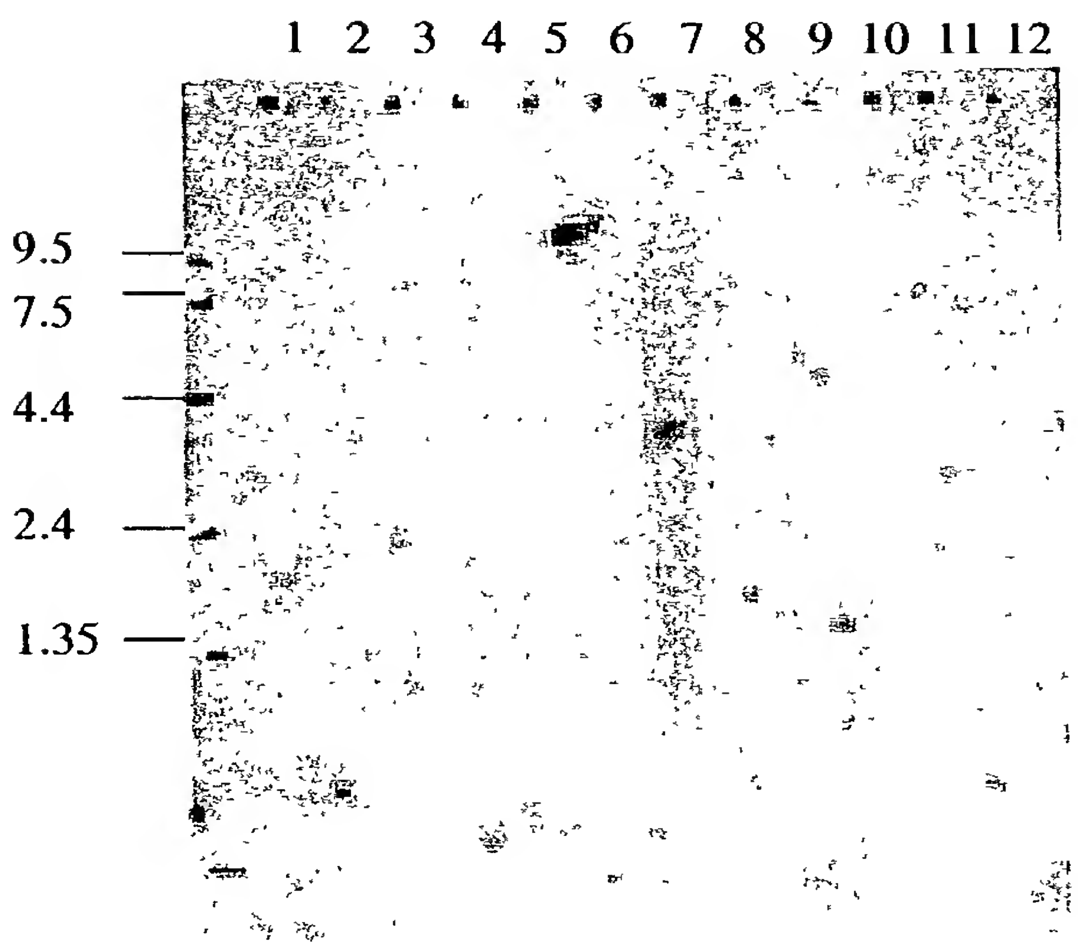
Gene 693



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

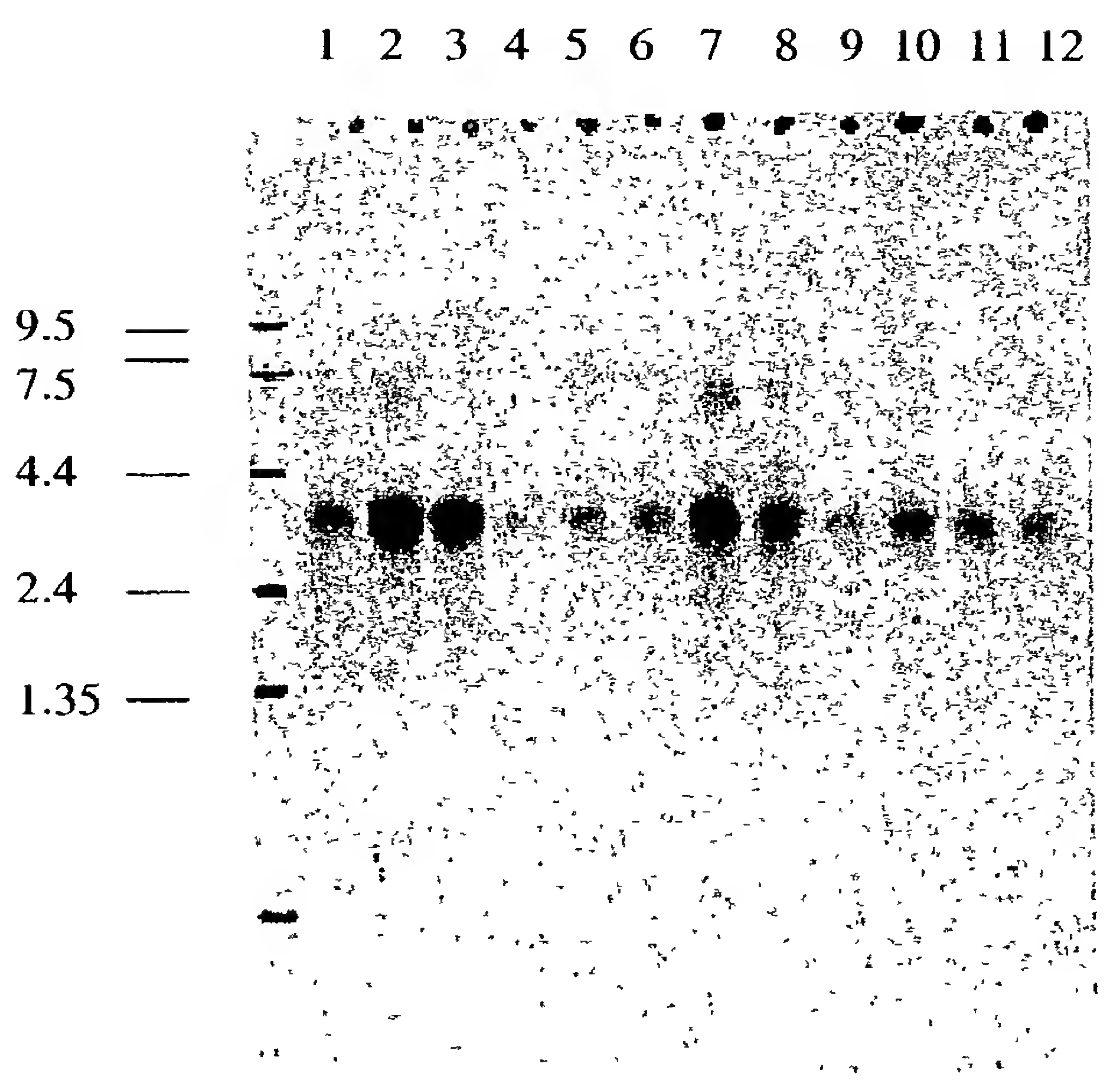
FIG. 6Q

Gene 698



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

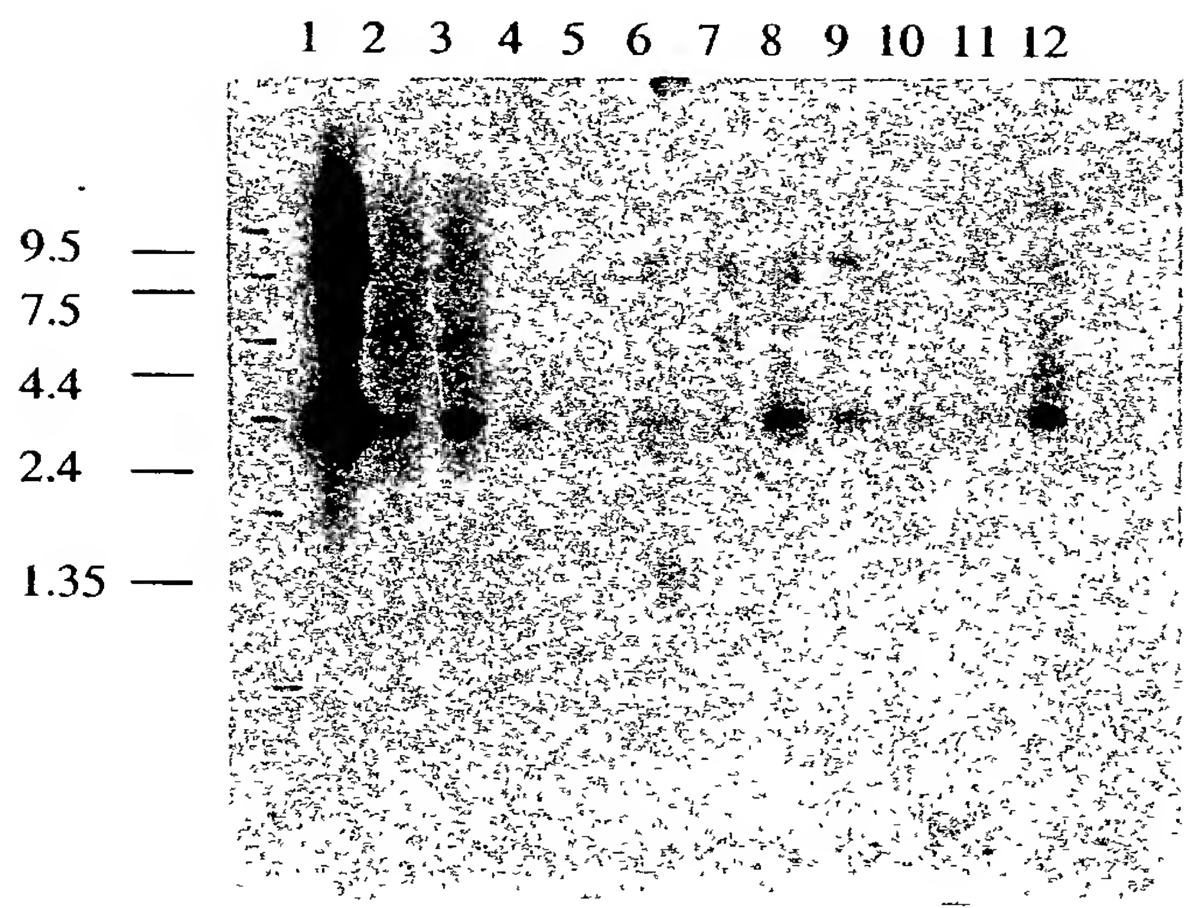
Gene 699



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

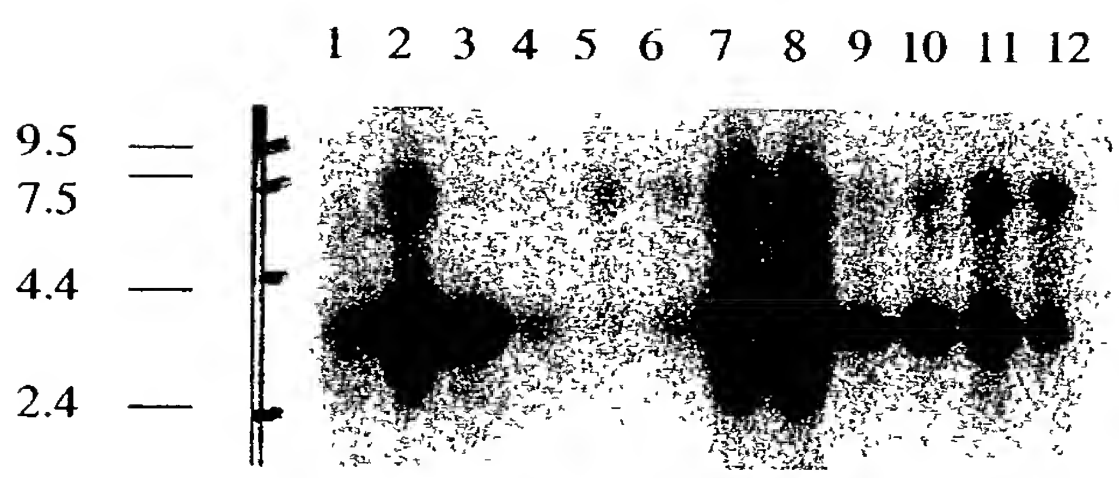
FIG. 6R

Gene 702



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

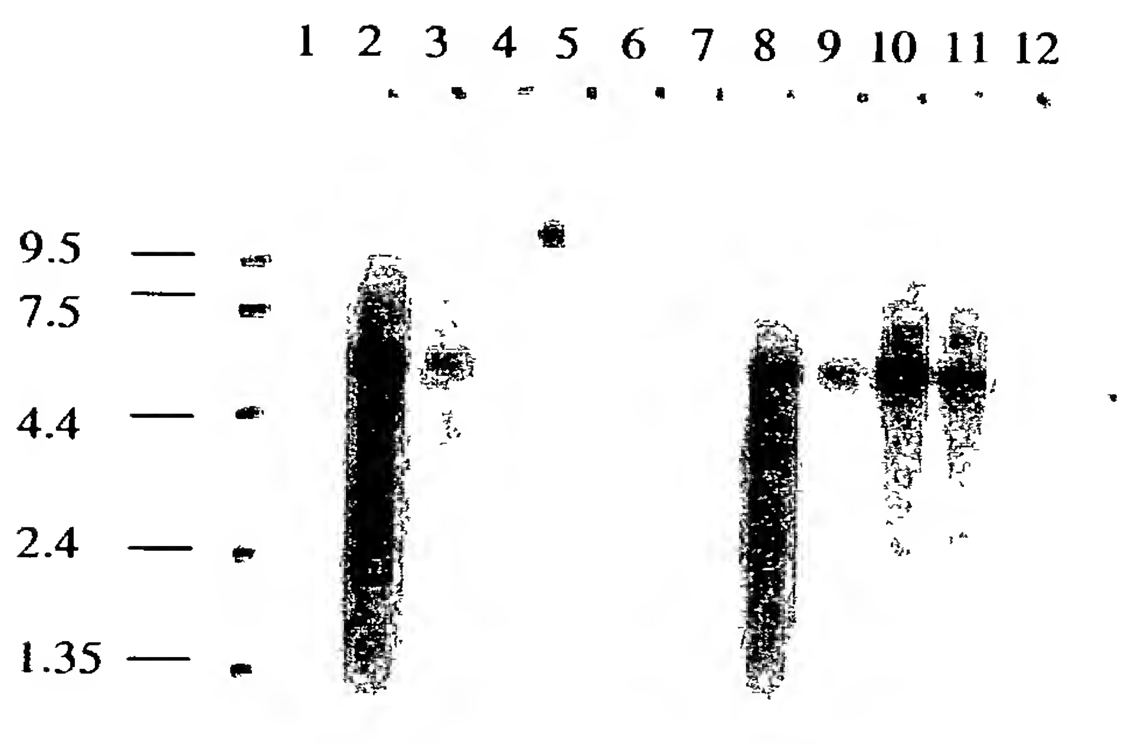
Gene 722



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

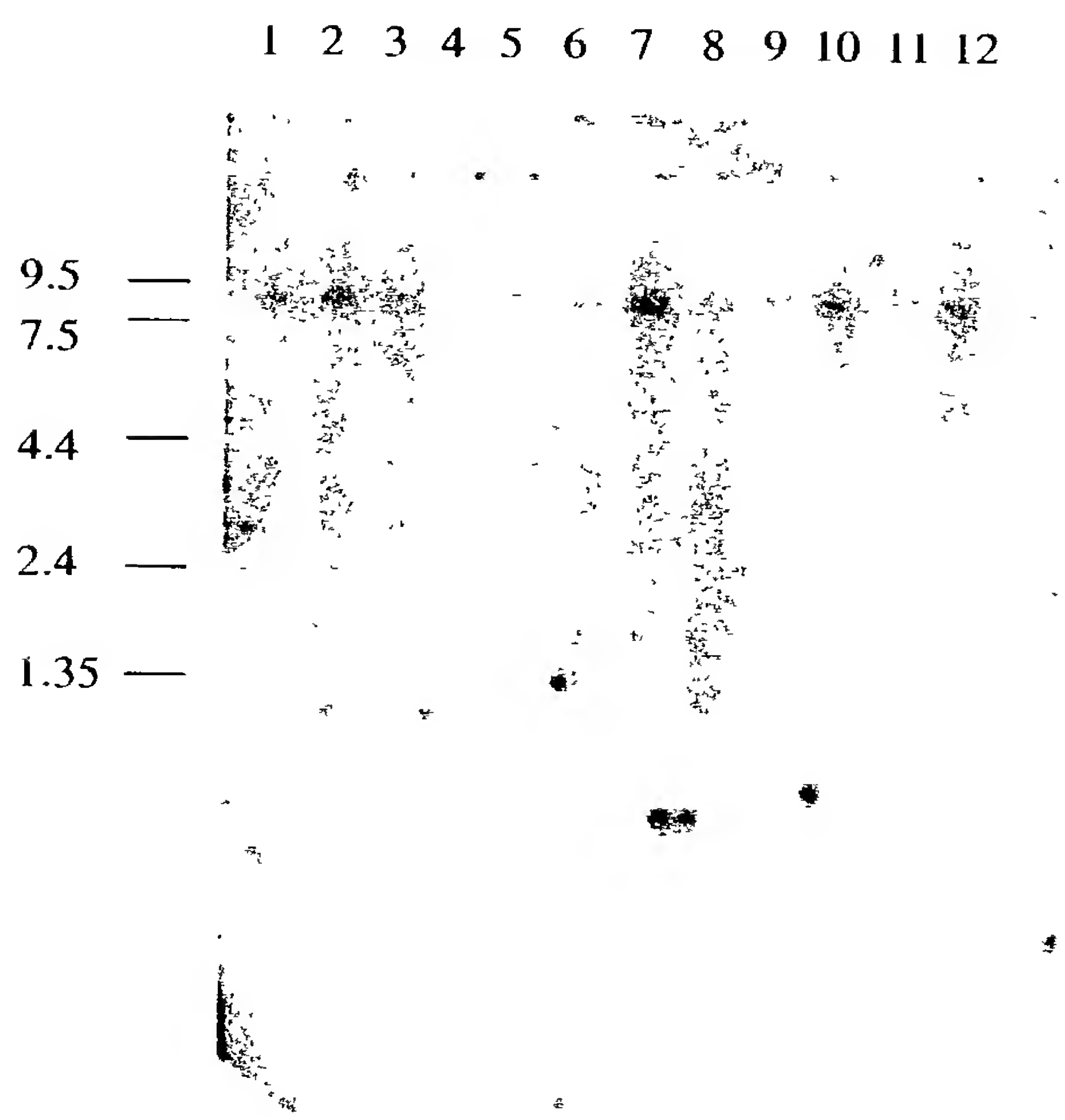
FIG. 6S

Gene 751



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

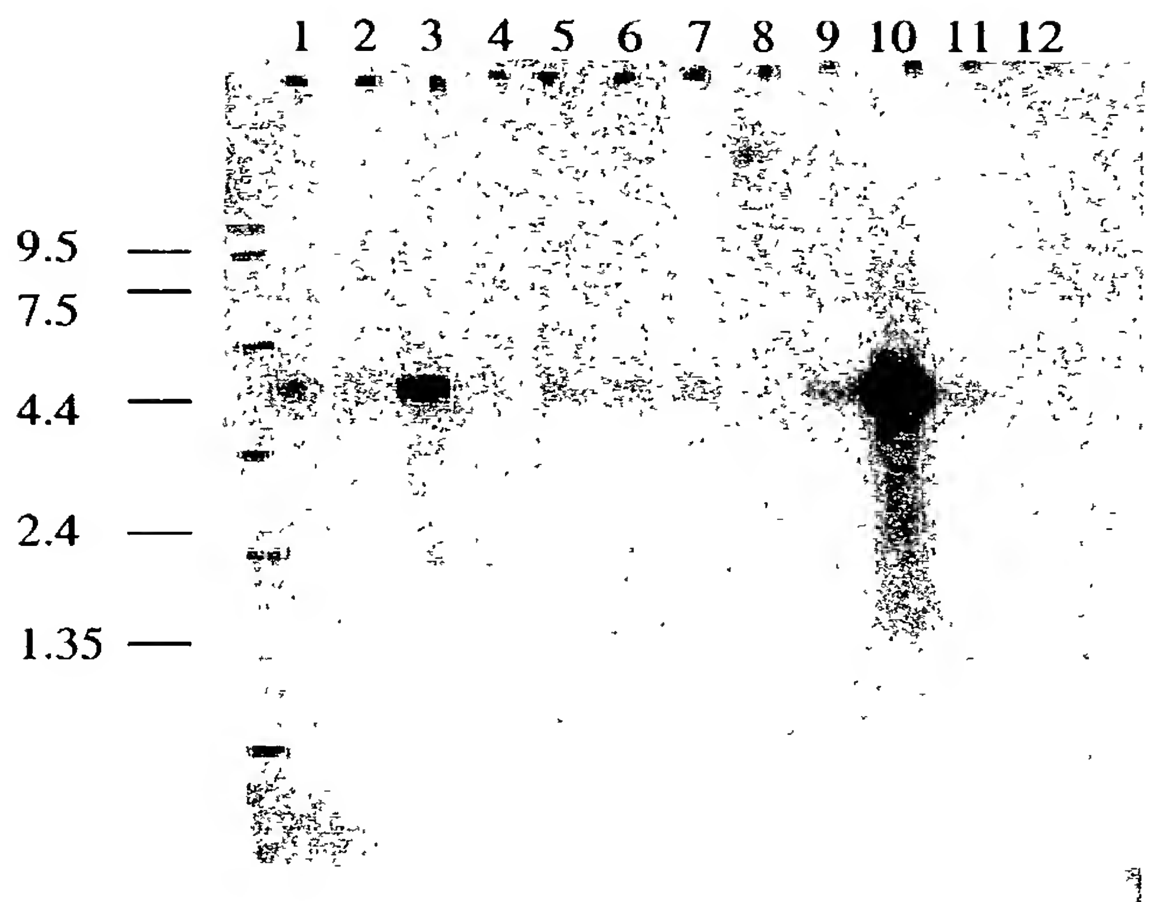
Gene 756



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

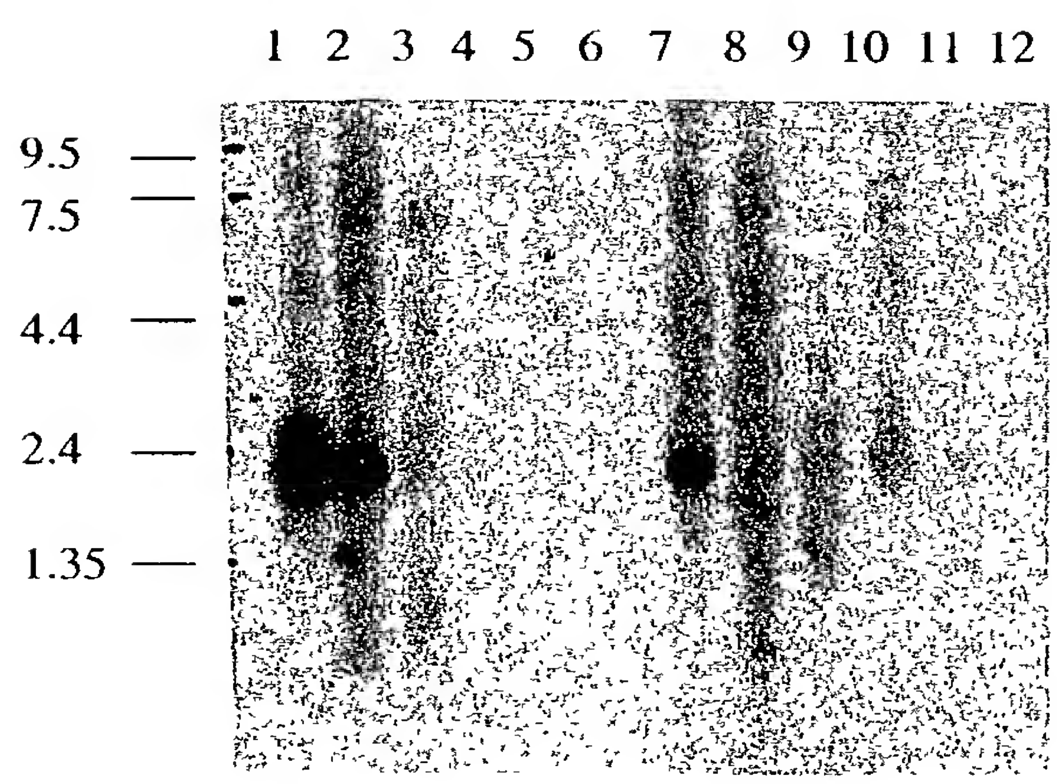
FIG. 6T

Gene 757



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

Gene 848



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6U

10 30 50

GCTTGCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCGCAGGGAGGGAG

70 90 110

GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCCAGTATGAGACGAACAAA
MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys

130 150 170

GTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGTGATCATC
ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle

190 210 230

TTTTCCTACGTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTC
PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal

250 270 290

ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCG<u>T</u>GGAG
IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIle<u>Val</u>Glu

310 330 350

AATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTG
AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu

370 390 410

CAGGGGAACTCTTTCTTCGTGATGACAAACTTTCTCAAAACAGAAGGCCAAGAGCAGCGG
GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg

430 450 470

TTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCCTCTGACCGAGGTTGTAAAAAG
LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys

490 510 530

GGATGGATGGACCCGCAGAGCAAAGGAATTCAGACC<u>G</u>GAAGGTGTGTAGTG<u>C</u>ATGAAGGG
GlyTrpMetAspProGlnSerLysGlyIleGlnThr<u>Gly</u>ArgCysValVal<u>His</u>GluGly

550 570 590

FIG. 7A

```
AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluGluAlaPro

      610                 630                 650
CGGCCTGCTCTCTTGAACAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

      670                 690                 710
TTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTTAAACATCACTTGTACC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

      730                 750                 770
TTCCACAAGACTCAGAATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

      790                 810                 830
ACAGGCGATAATTTTTCAGATGTGGCAATTCAGGGCGGAATAATGGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

      850                 870                 890
TGGGACTGCAACCTAGACCGTTGGTTCCATCACTGCCGTCCCAAATACAGTTTCCGTCGC
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

      910                 930                 950
CTTGACGACAAGACCACCAACGTGTCCTTGTACCCTGGCTACAACTTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

      970                 990                 1010
TACTACAAGGAAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTTCGGGATCCGTTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

      1030                1050                1070
GACATCCTGGTTTTTGGCACCGGAGGAAAATTTGACATTATCCAGCTGGTTGTGTACATC
AspIleLeuValPheGlyThrGlyGlyLysPheAspIleIleGlnLeuValValTyrIle

      1090                1110                1130
GGCTCAACCCTCTCCTACTTCGGTCTGGCCACTGTGTTCATCGACTTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr
```

FIG. 7B

```
     1150                1170                1190
        .         .         .         .         .         .
TACTCCAGTAACTGCTGTCGCTCCCATATTTATCCCTGGTGCAAGTGCTGTCAGCCCTGT
TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

     1210                1230                1250
        .         .         .         .         .         .
GTGGTCAACGAATACTACTACAGGAAGAAGTGCGAGTCCATTGTGGAGCCAAAGCCGACA
ValValAsnGluTyrTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

     1270                1290                1310
        .         .         .         .         .         .
TTAAAGTATGTGTCCTTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA
LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

     1330                1350                1370
        .         .         .         .         .         .
GGGAGAAGTTTGCAAGATGTCAAGGGCCAAGAAGTCCCAAGACCTGCGATGGACTTCACA
GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

     1390                1410                1430
        .         .         .         .         .         .
GATTTGTCCAGGCTGCCCCTGGCCCTCCATGACACACCCCCGATTCCTGGACAACCAGAG
AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

     1450                1470                1490
        .         .         .         .         .         .
GAGATACAGCTGCTTAGAAAGGAGGCGACTCCTAGATCCAGGGATAGCCCCGTCTGGTGC
GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

     1510                1530                1550
        .         .         .         .         .         .
CAGTGTGGAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG
GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluGluLeu

     1570                1590                1610
        .         .         .         .         .         .
TGCTGCCGGAAAAAGCCGGGGGCCTGCATCACCACCTCAGAGCTGTTCAGGAAGCTGGTC
CysCysArgLysLysProGlyAlaCysIleThrThrSerGluLeuPheArgLysLeuVal

     1630                1650                1670
        .         .         .         .         .         .
CTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT
LeuSerArgHisValLeuGlnPheLeuLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

     1690                1710                1730
        .         .         .         .         .         .
```

FIG. 7C

GTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750 1770 1790

TTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTGCCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810 1830 1850

CGGAAAGAGTTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTCAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870 1890 1910

CAGGCACCGTGGCTCACGTCTGTAATCCCAGCGCTTTGGGAGGCCGAGGCAGGCAGATCA

1930 1950 1970

CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAGGCGAAATCCTGTCTGTACTAAA

1990 2010 2030

AATACAAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050 2070 2090

GAGGCACAAGAATCACTTGAACCCGGGAGGCAGAGGTTGTAGTGAGCCCAGATTGTGCCA

2110 2130 2150

CTGCTCTCCAGCCTGGGAGGCACAGCAAACTGTCCCAAAAAAAAAAAAAAGAGTCCTTAC

2170 2190 2210

CAATAGCAGGGGCTGCAGTAGCCATGTTAACATGACATTTACCAGCAACTTGAACTTCAC

2230 2250 2270

CTGCAAAGCTCTGTGGCCACATTTTCAGCCAAAGGGAAATATGCTTTCATCTTCTGTTGC

2290 2310 2330

TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAAACCAGAATCCCTCTACATGGACT

2350 2370 2390

FIG. 7D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCTA

2410 2430 2450

GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTTGCCCAACTACTATCTCAGAGATATTGT

2470 2490 2510

GAGGACAAATTGAGACAGTGCACATGAACTGTCTTTTAATGTGTAAAGATCTACATGAAT

2530 2550 2570

GCAAAACATTTCATTATGAGGTCAGACTAGGATAATGTCCAACTAAAAACAAACCCTTTT

2590 2610 2630

CATCCTGGCTGGAGAATGTGGAGAACTAAAGGTGGCCACAAATTCTTTGACACTCAAGTC

2650 2670 2690

CCCCAAGACCTAAGGGTTTTATCTCCTCCCCTTGAATATGGGTGGCTCTGATTGCTTTAT

2710 2730 2750

CCAAAAGTGGAAGTGACATTGTGTCAGTTTCAGATCCTGATCTTAAGAGGCTGACAGCTT

2770 2790 2810

CTACTTGCTGTCCCTTGGAACTCTTGCTATCGGGGAAGCCAGACGCCATTTAAAAGTCTG

2830 2850 2870

CCTATCCTGGCCAGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCAAGG

2890 2910 2930

CGGGCGGATCACTTAAAGTCAGGAGTCCAAGACCAGACTCGCCAACATGGTGAAACCGTA

2950 2970 2990

TCTCTAATAAAAATACAAAAATTAGCTGGGCATGGTGCGGGCACCTGTAGTCCTAGCTAT

3010 3030 3050

CAAGAGGCTGAGACAGGAGAAACACTTGAACCTGGGAGGTGGAGGTTGCATTGAGCTGAG

FIG. 7E

```
   3070                3090                3110
      .         .         .         .         .         .
ATCGTGCCACTGCACTCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAAAA

   3130                3150                3170
      .         .         .         .         .         .
AAAAGAAAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCAAGCA

   3190                3210                3230
      .         .         .         .         .         .
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTTCAAGCCATCCAAGCCCAGTCACCAAA

   3250                3270                3290
      .         .         .         .         .         .
CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATACCGC

   3310                3330                3350
      .         .         .         .         .         .
ATGATACATCCCAAGTGAGAACTGCCCCATAAATCCAGAAAACCACATTGCTATCTTAAG

   3370                3390                3410
      .         .         .         .         .         .
TCCCTAAGTTTGGGGCTTATTTGTTCCACAGCAACAGGTAACTGGAACAGAGGGCAAGCC

   3430                3450                3470
      .         .         .         .         .         .
TGATGAATGGGCACACAGACTCAGCCCATACCTTCCCTGGTTCTAATGTTCTCAGGGAGC

   3490                3510                3530
      .         .         .         .         .         .
CCGGACCAACCCTGGGAGCCTCAGGAACTTAGGTTTCCACTGGACAGTTCTAGAAGGGCT

   3550                3570                3590
      .         .         .         .         .         .
ATAGACCAAATCAGGTAACTCACCAGACCAGCCTTGGAATCTATCAAATCTAACTGCTGA

   3610                3630                3650
      .         .         .         .         .         .
GCTACCCAGTGCATTCCGATCCTCATCACAATTCTTTGACTGAAGGCCGGGCGTGGTGGC

   3670                3690                3710
      .         .         .         .         .         .
TCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTCAGGA
```

FIG. 7F

3730 3750 3770

GTTCGAGACCAGCCTGGCCAACATGGTGAGACCCTGTCTCTACTAAGAATACAAAAATTA

3790 3810 3830

GGTGGGGTGGCGGTGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATC

3850 3870 3890

TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT

3910 3930 3950

AGATAACAGAGCAAGACTCTGTCTCAAAAAACAACAACAACAACAACAAAACAATTCTAT

3970 3990 4010

GACTGAAAGTGACTAAAAAGCTGGCTTTATGCCATTAACACTCTGTACTTTGCAGCCAAT

4030 4050 4070

CAGAACTGACGCAGTCTGGGTGCTAGCTGCTTCAAAAGCAACCCACACCACACTTTTACC

4090 4110 4130

ATTTCCATACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTTTAGGATCCTG

4150 4170 4190

CTTCAGGATTTCCTTTTCCTGGTTTGGTCACTAGAGTTGGCTATTTATCTGTTTCTAAAC

4210 4230 4250

AATAGCTATTTTATCGAATAGTTTAGAGACCACTATTAAATATTGTGACTGATGAAGGAT

4270 4290 4310

CTGTGAATTTTTTTATATATGTTCTAAGAGTTACCATTTTGATACCTTTTAAAAACCAGC

4330 4350 4370

AGCTTTCTACTATATTCATGTAAAACAGCATGAATAAAACCATTTTTGATACAGGGTTT

4390 4410 4430

FIG. 7G

TATTTGGCTTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTTGATTTTTACT

4450 4470 4490

ACCTTTTCAAAGATATTTTAAAAAGTGGATTACTACATATGATTTCTTTGGAGCTTACAT

4510 4530 4550

TTCTTTACTTCACGAATTCTATGTCACTGTTACAAGTTTCCATTCTGATGGCTTCTGGGC

4570 4590 4610

CTTTGTACCTTTGTTTTTGGTGCCTTATTCCTAGTATGTTTCTATCACCTTAATGAGGCC

4630 4650 4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTTTCCAT

4690 4710 4730

CACCTTCCCCACTGATGCTCTGGGCGAGAGAGTGATGTGTCACTTCAACTGTGTGTAATA

4750 4770 4790

TGTCAGACACGTCCTACAATAACAGGCGTCATATTTGTATTATTTTTAGTTTACTGTAGA

4810 4830 4850

AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTTTGTAGGATCTGTTTTCTTATAC

4870 4890 4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTCATGGCTTCCTTTCTGTGTCAGA

4930 4950 4970

AGAGAAGGGATCTGCTTTCTCTTGGCTGATTTCACATAGCATTGGTAATAGACATGCATT

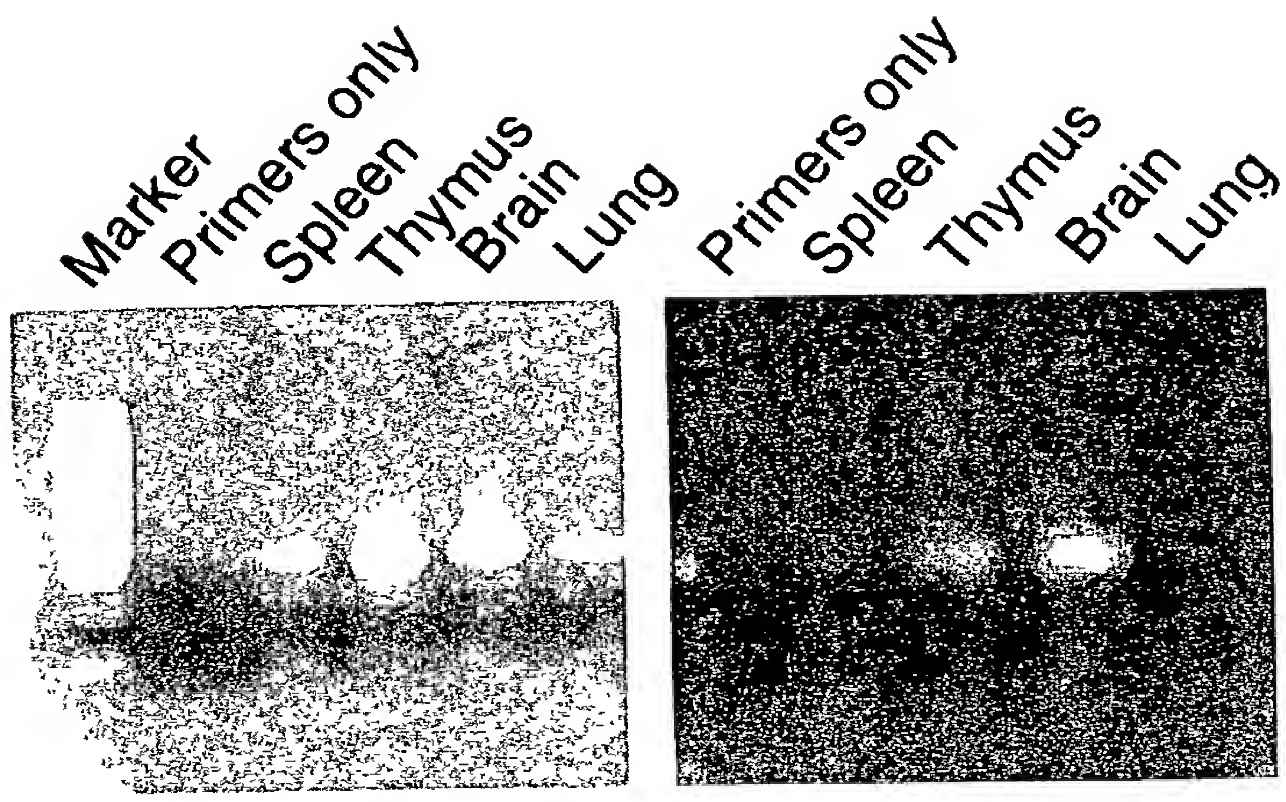
4990 5010 5030

TCTCTTTCTAAAGGGGAGTAACTTTTTAAACCCTTCCTGATTTTAGCCTGGCAATGTAAG

5050 5070

TGTCCTTAATGTGACTGTTTTGATAATTAAAAAAAGGTATATAATTT

FIG. 7H



Gene561.nt1 Gene561.nt2

RT/PCR of Gene561.nt1 and Gene561.nt2

FIG. 8

10 30 50

TCGAAACAGCTGCCGGCTGGTCCCGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCCGG

70 90 110

GCTGTGGGGGCGCCGCGAGCTGGGCCGGCCTCGGTGTGCCCGCGCCGCCAGCCCGCTCCA

130 150 170

GACGCGCCACCTGGGCGCTCCAAGAAGAGGCCGAAGTTTGCCGCGGCCGTGAGTTGGAGC

190 210 230

TCGCGCCGGGCCGCTGCGCCGGGAGCTCCGGGGGCTTCCCTCGCTTCCCGGTATTGTTTG

250 270 290

CAAACTTTGCTGCTCTCCGCCGCGGCCCCCAACTCGGCGGACGCCGGGCGCGGAGAGCCG

310 330 350

AGCCGGGGGCGCTGTGCGCAGCGCTCGGGCCAGGCCGGGCGGGCATGGGCGGGGGCCCGA

370 390 410

GCAGGGGTGGAGAGCCGGGGCCAGCAGCAGCCCGTGCCCGGGAGCGGCGGCGCTGAGGGG

430 450 470

CGCGGAGCTCCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCCGGGCCCCCGCCTG
MetGlnArgProGlyProArgLeu

490 510 530

TGGCTGGTCCTGCAGGTGATGGGCTCGTGCGCCGCCATCAGCTCCATGGACATGGAGCGC
TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg

550 570 590

CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCCGATGTGCAAGGACATCGGCTACAAC
ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn

610 630 650

FIG. 9A

```
ATGACTCGTATGCCCAACCTGATGGGCCACGAGAACCAGCGCGAGGCAGCCATCCAGTTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

      670                 690                 710

CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

      730                 750                 770

TCGCTGTACGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCCGCCTGCCGGGTC
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

      790                 810                 830

ATGTGCGAGCAGGCCCGGCTCAAGTGCTCCCCGATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

      850                 870                 890

CCCGACTCCCTGGACTGCCGGAAACTCCCCAACAAGAACGACCCCAACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

      910                 930                 950

GAGGCGCCCAACAACGGCTCGGACGAGCCCACCCGGGGCTCGGGCCTGTTCCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

      970                 990                1010

TTCCGGCCGCAGCGGCCCCACAGCGCGCAGGAGCACCCGCTGAAGGACGGGGGCCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

     1030                1050                1070

CGCGGCGGCTGCGACAACCCGGGCAAGTTCCACCACGTGGAGAAGAGCGCGTCGTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

     1090                1110                1130

CCGCTCTGCACGCCCGGCGTGGACGTGTACTGGAGCCGCGAGGACAAGCGCTTCGCAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

     1150                1170                1190
```

FIG. 9B

GTCTGGCTGGCCATCTGGGCGGTGCTGTGCTTCTTCTCCAGCGCCTTCACCGTGCTCACC

ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210 1230 1250

TTCCTCATCGACCCGGCCCGCTTCCGCTACCCCGAGCGCCCCATCATCTTCCTCTCCATG

PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270 1290 1310

TGCTACTGCGTCTACTCCGTGGGCTACCTCATCCGCCTCTTCGCCGGCGCCGAGAGCATC

CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330 1350 1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC

AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390 1410 1430

TGCACGCTGGTCTTCCTGGTCCTCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGGTG

CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450 1470 1490

GTCCTCACGCTCACCTGGTTCCTGGCCGCCGGCAAGAAGTGGGGCCACGAGGCCATCGAA

ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510 1530 1550

GCCAACAGCAGCTACTTCCACCTGGCAGCCTGGGCCATCCCGGCGGTGAAGACCATCCTG

AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570 1590 1610

ATCCTGGTCATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGGTCTGCTACGTGGGCAGC

IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630 1650 1670

ATGGACGTCAACGCGCTCACCGGCTTCGTGCTCATTCCCCTGGCCTGCTACCTGGTCATC

MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690 1710 1730

FIG. 9C

```
GGCACGTCCTTCATCCTCTCGGGCTTCGTGGCCCTGTTCCACATCCGGAGGGTGATGAAG
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

       1750                 1770                 1790

ACGGGCGGCGAGAACACGGACAAGCTGGAGAAGCTCATGGTGCGTATCGGGCTCTTCTCT
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

       1810                 1830                 1850

GTGCTGTACACCGTGCCGGCCACCTGTGTGATCGCCTGCTACTTTTACGAACGCCTCAAC
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

       1870                 1890                 1910

ATGGATTACTGGAAGATCCTGGCGGCGCAGCACAAGTGCAAAATGAACAACCAGACTAAA
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

       1930                 1950                 1970

ACGCTGGACTGCCTGATGGCCGCCTCCATCCCCGCCGTGGAGATCTTCATGGTGAAGATC
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

       1990                 2010                 2030

TTTATGCTGCTGGTGGTGGGGATCACCAGCGGGATGTGGATTTGGACCTCCAAGACTCTG
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

       2050                 2070                 2090

CAGTCCTGGCAGCAGGTGTGCAGCCGTAGGTTAAAGAAGAAGAGCCGGAGAAAACCGGCC
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysLysSerArgArgLysProAla

       2110                 2130                 2150

AGCGTGATCACCAGCGGTGGGATTTACAAAAAAGCCCAGCATCCCCAGAAAACTCACCAC
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

       2170                 2190                 2210

GGGAAATATGAGATCCCTGCCCAGTCGCCCACCTGCGTGTGAACAGGGCTGGAGGGAAGG
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

       2230                 2250                 2270
```

FIG. 9D

GCACAGGGGCGCCCGGAGCTAAGATGTGGTGCTTTTCTTGGTTGTGTTTTTCTTTCTTCT

2290 2310 2330

TCTTCTTTTTTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAAGTGTTTACCCTG

2350 2370 2390

AAATTCAGGATGCTGTGATACACTGAAAGGAAAAATGTACTTAAAGGGTTTTGTTTTGTT

2410 2430 2450

TTGGTTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTTGTGTAACTAATTTGT

2470 2490 2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACTTTTGTTTAGAGCCCTCCSTAAATAT

2530 2550 2570

ACATCTGTGTATTTGAGTTGGCTTTGCTACCCATTTACAAATAAGAGGACAGATAACTGC

2590 2610 2630

TTTGCAAATTCAAGAGCCTCCCCTGGGTTAACAAATGAGCCATCCCCAGGGCCCACCCCC

2650 2670 2690

AGGAAGGCCACAGTGCTGGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCCGCC

2710 2730 2750

TCACACCCCAGTGGATTTGGAGTTGCTTAAAATAGACTCCGGCCTTCACCAATAGTCTCT

2770 2790 2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTTGTGAACTCAAACGATGTGCAATACA

2830 2850 2870

TTTTTTTCTCTTTCCTTGAAAATAAAAAGAGAAACAAGTATTTTGCTATATATAAAGACA

2890 2910 2930

FIG. 9E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCCAGCCCTCAGAAACCCTTCAGTGC

2950 2970 2990

TACATTTTGTGGCTTTTTAATGGAAACCAAGCCAATGTTATAGACGTTTGGACTGATTTG

3010 3030 3050

TGGAAAGGAGGGGGGAAGAGGGAGAAGGATCATTCAAAAGTTACCCAAAGGGCTTATTGA

3070 3090 3110

CTCTTTCTATTGTTAAACAAATGATTTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3130 3150 3170

AGACACTTTGTCTAGTGTATTCTCTTCACAGTGCCAGGAAAGAGTGGTTTCTGCGTGTGT

3190 3210 3230

ATATTTGTAATATATGATATTTTTCATGCTCCACTATTTTATTAAAAATAAAATATGTTC

3250

TTTAGTTTGCTGCT

FIG. 9F

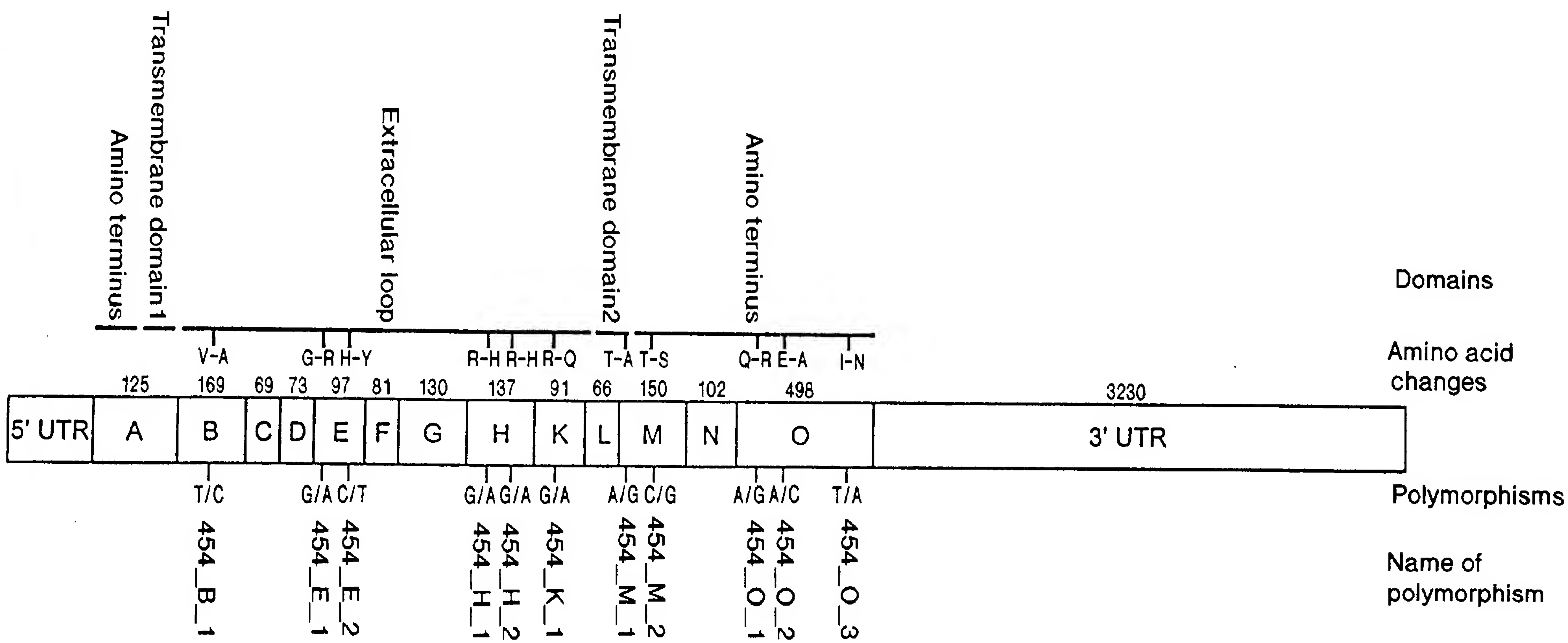
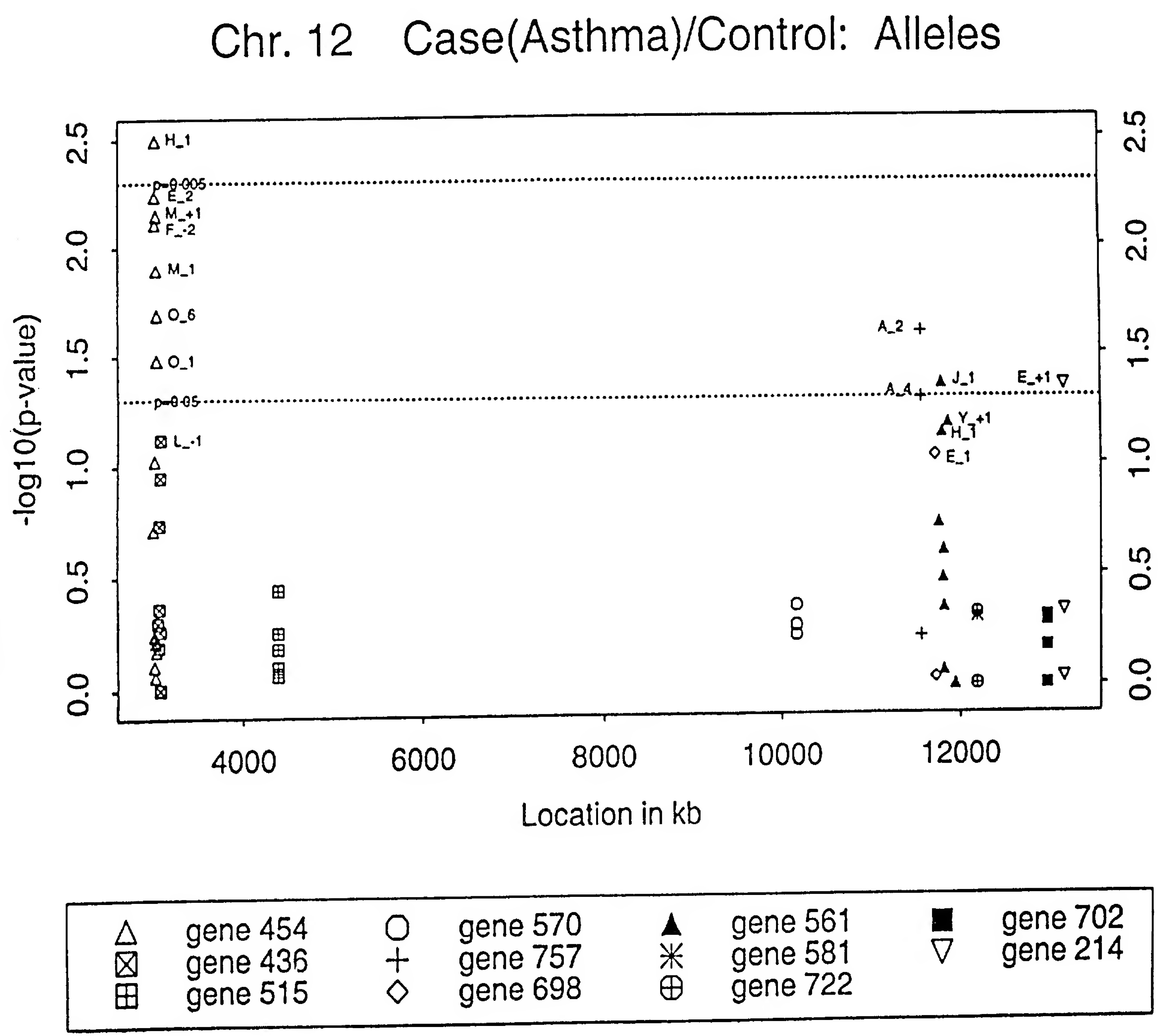

Amino terminus
Transmembrane domain1
Extracellular loop
Transmembrane domain2
Amino terminus
Domains
V-A
G-R H-Y
R-H R-H R-Q
T-A T-S
Q-R E-A
I-N
Amino acid changes
125
169
69
73
97
81
130
137
91
66
150
102
498
3230
5' UTR
A
B
C
D
E
F
G
H
K
L
M
N
O
3' UTR
T/C
G/A C/T
G/A G/A G/A
A/G C/G
A/G A/C
T/A
Polymorphisms
454_B_1
454_E_1
454_E_2
454_H_1
454_H_2
454_K_1
454_M_1
454_M_2
454_O_1
454_O_2
454_O_3
Name of polymorphism

FIG. 10



Chr. 12 Case(Asthma)/Control: Alleles
-log10(p-value)
0.0
0.5
1.0
1.5
2.0
2.5
Location in kb
4000
6000
8000
10000
12000
p=0.005
p=0.05
H_1
E_2
M_+1
F_-2
M_1
O_6
O_1
L_-1
A_2
A_4
J_1
Y_+1
H_1
E_1
E_+1
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 581
gene 722
gene 702
gene 214

FIG. 11

Chr. 12 Case(Asthma)/Control: Alleles

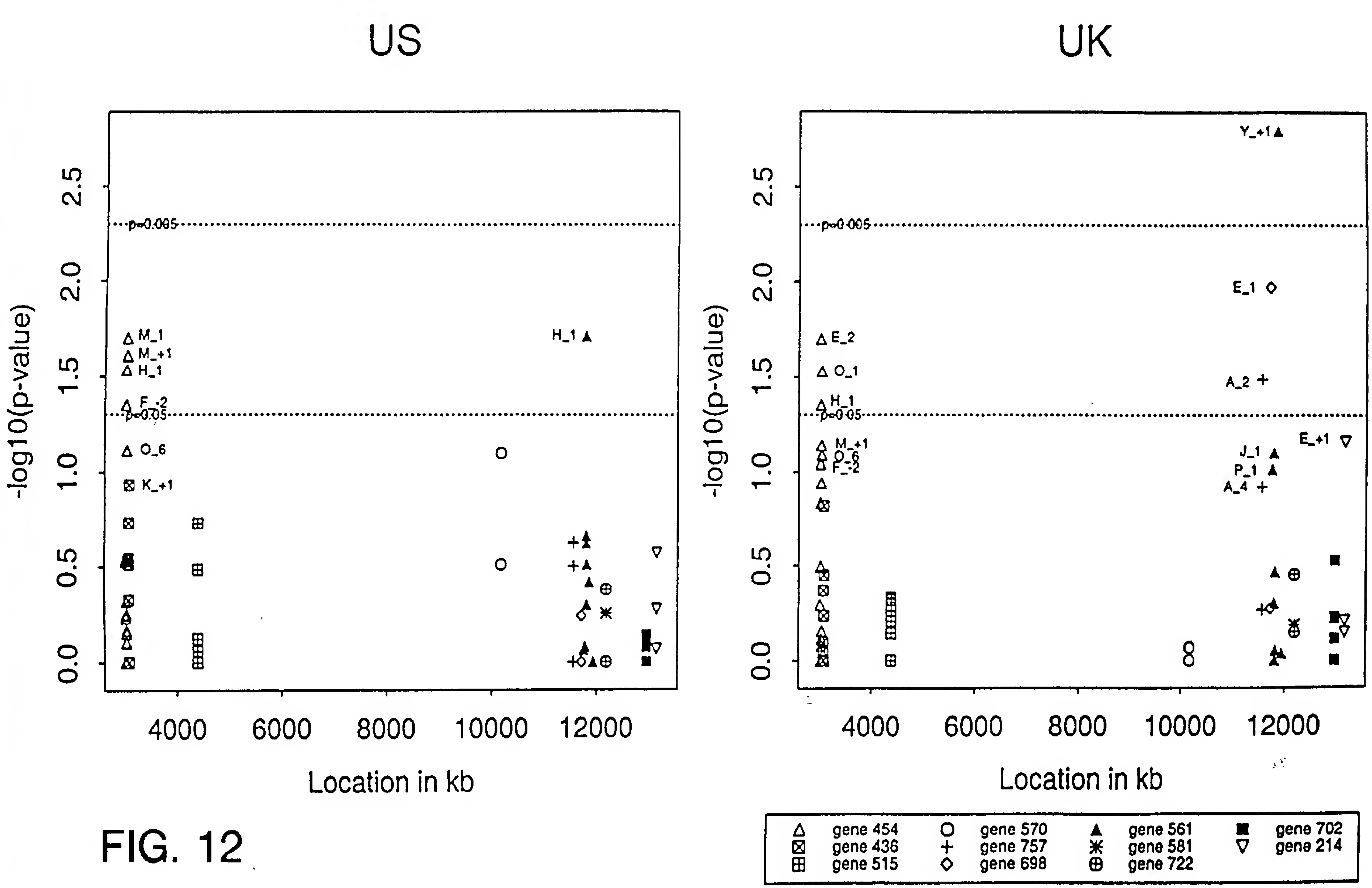


FIG. 12

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

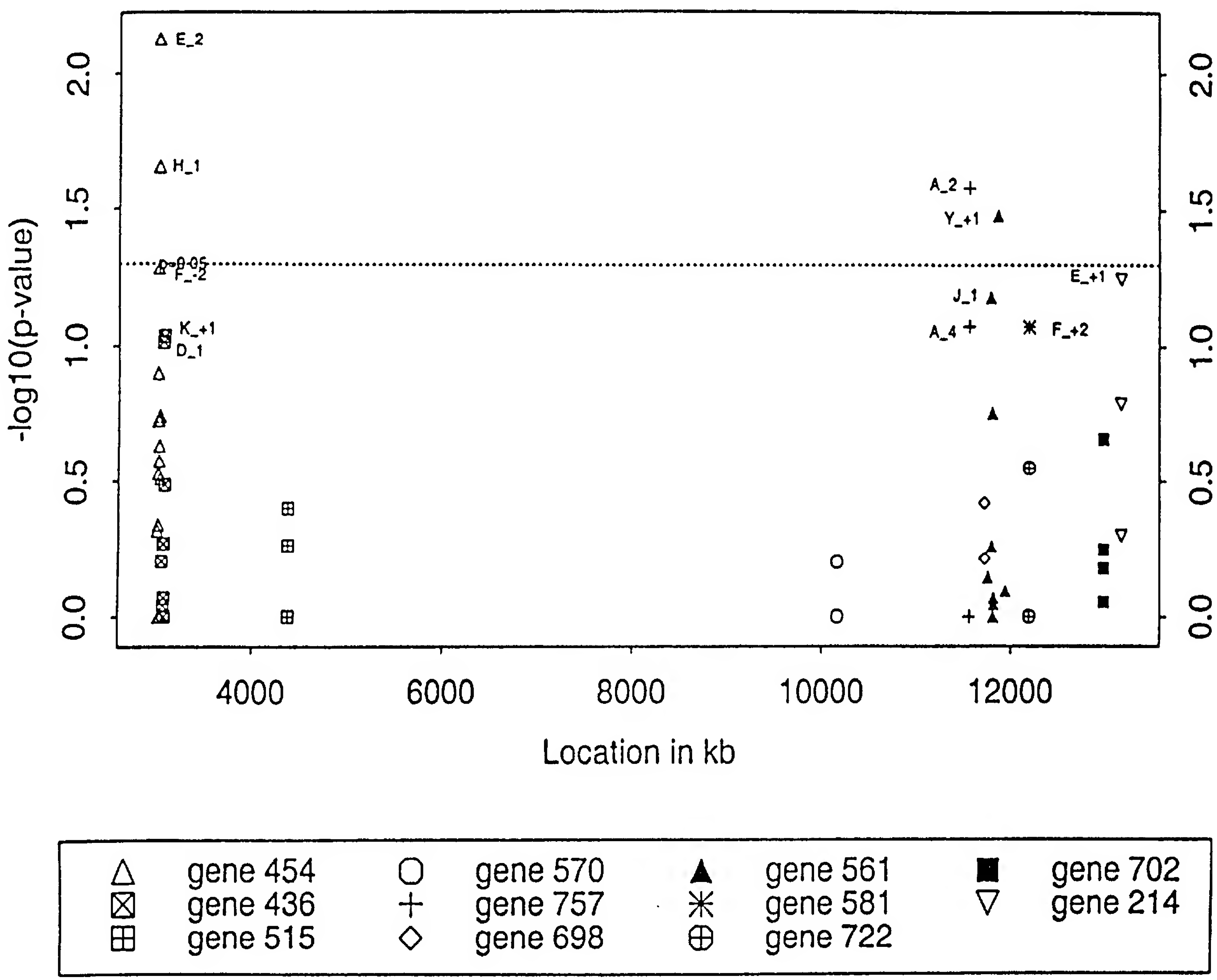


FIG. 13

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Alleles

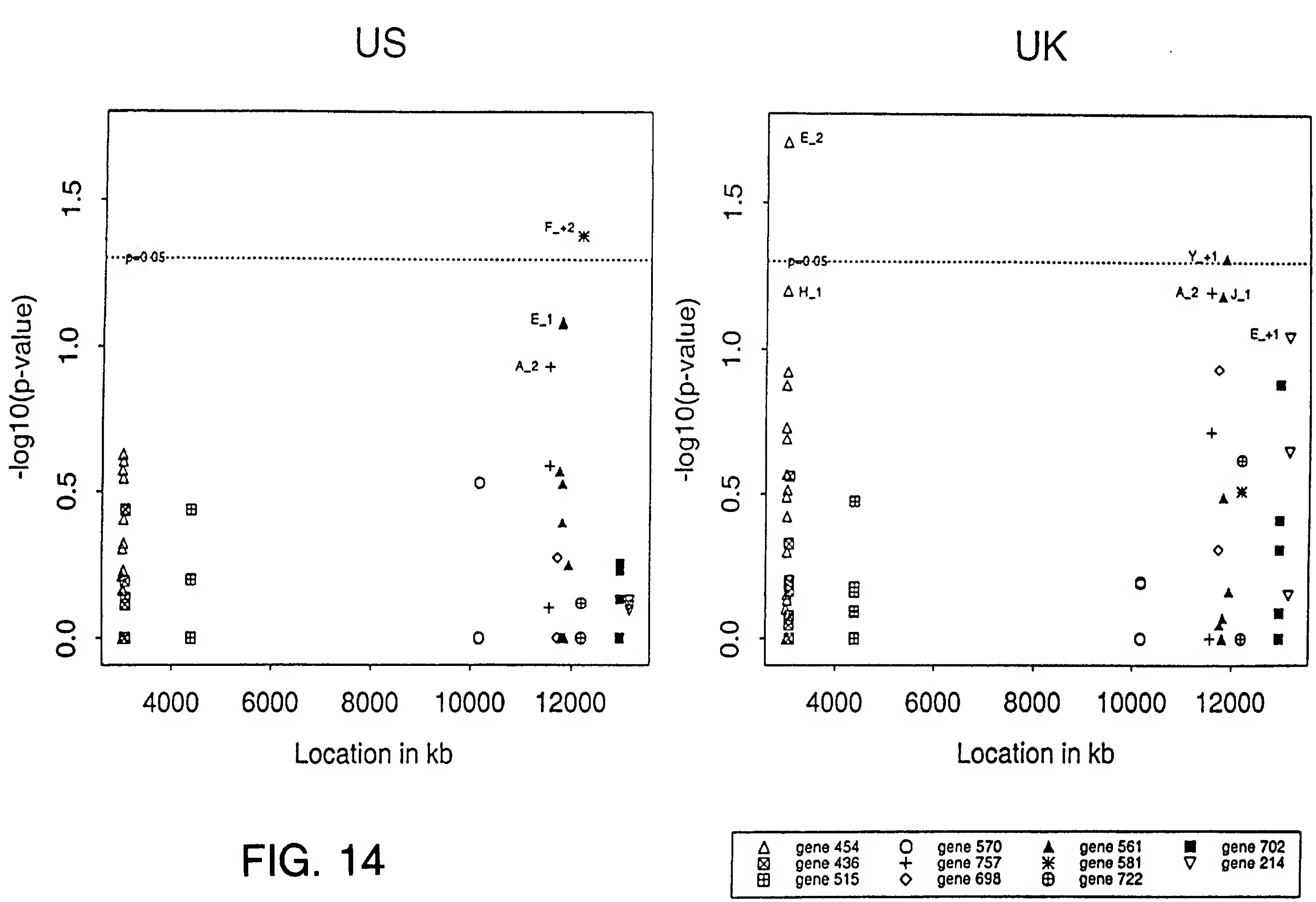
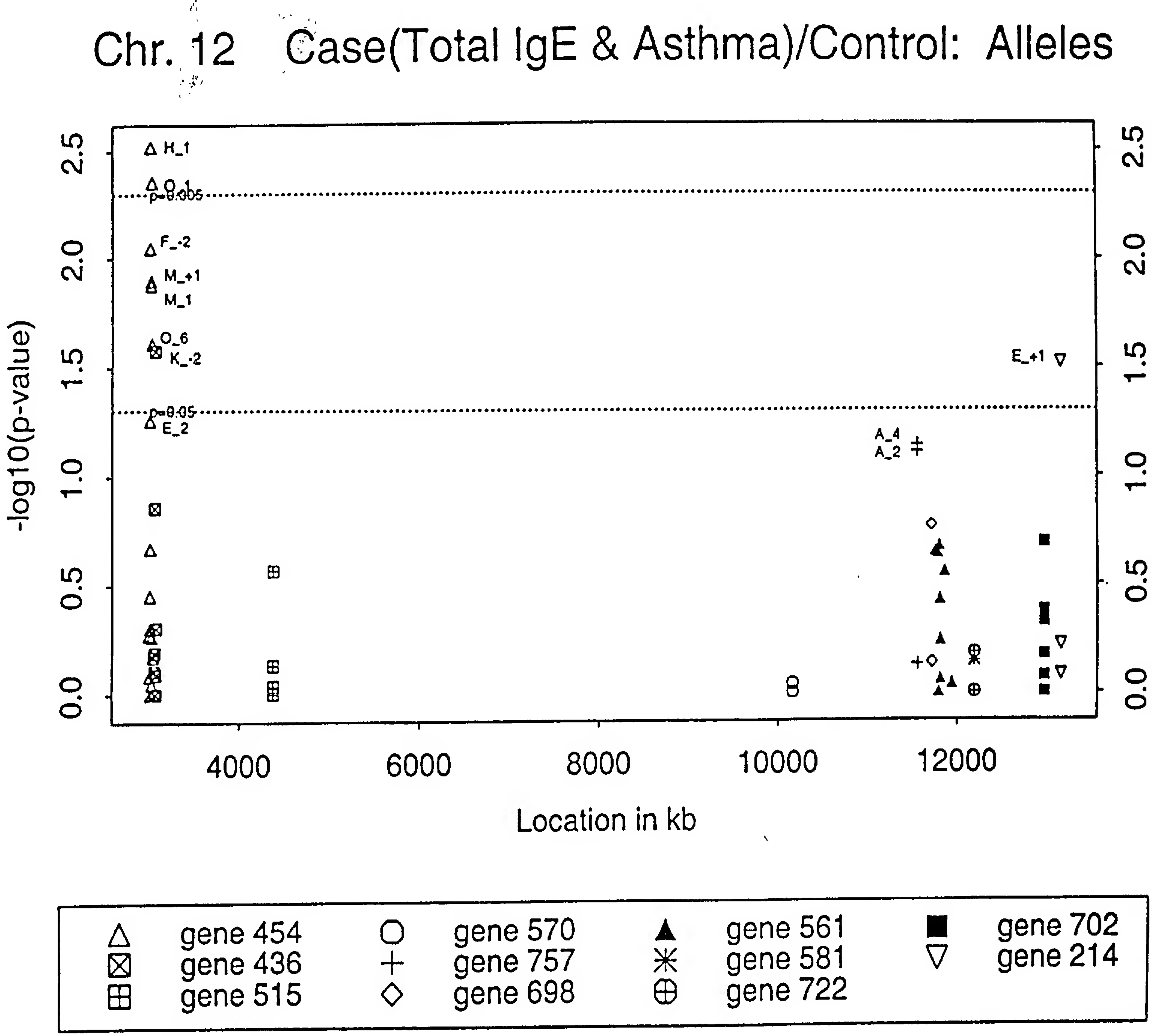


FIG. 14



Chr. 12 Case(Total IgE & Asthma)/Control: Alleles
-log10(p-value)
Location in kb
p=0.005
p=0.05
H_1
O_1
F_-2
M_+1
M_1
O_6
K_-2
E_2
A_4
A_2
E_+1
0.0
0.5
1.0
1.5
2.0
2.5
4000
6000
8000
10000
12000
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 581
gene 722
gene 702
gene 214

FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

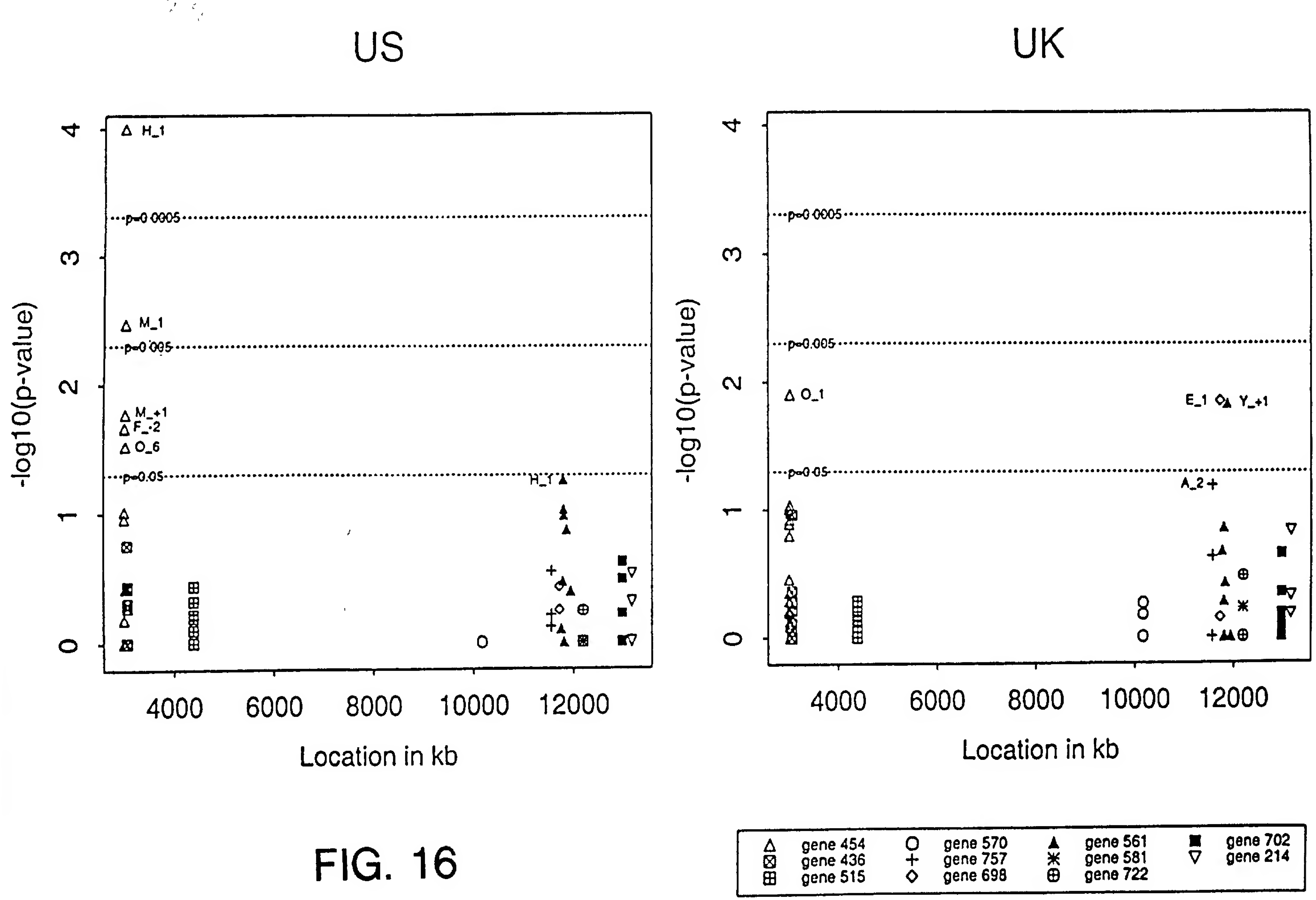


FIG. 16

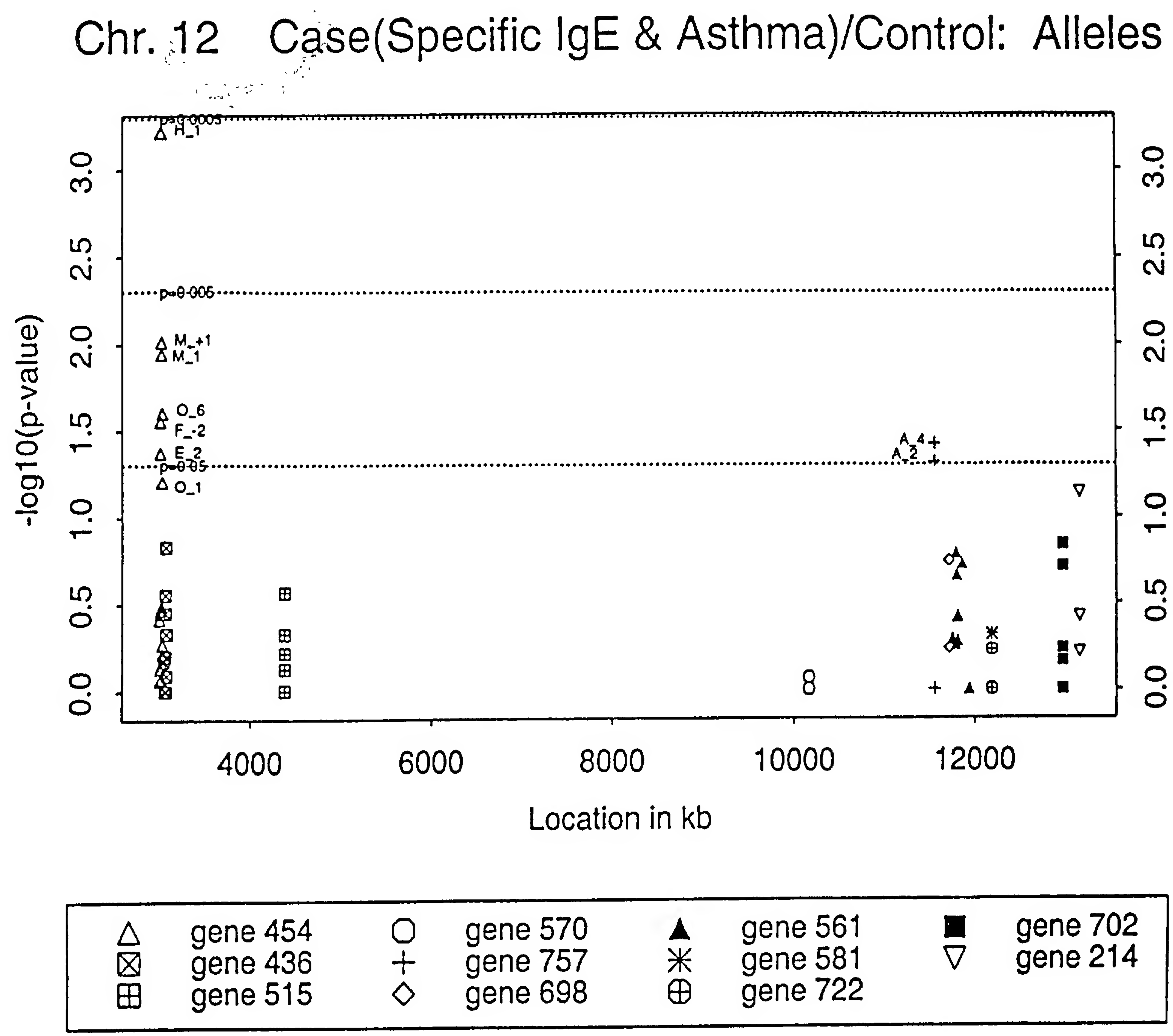

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles
-log10(p-value)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
p=0.0005
H_1
p=0.005
M_+1
M_1
O_6
F_-2
E_2
p=0.05
O_1
A_4
A_2
4000
6000
8000
10000
12000
Location in kb
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 581
gene 722
gene 702
gene 214

FIG. 17

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

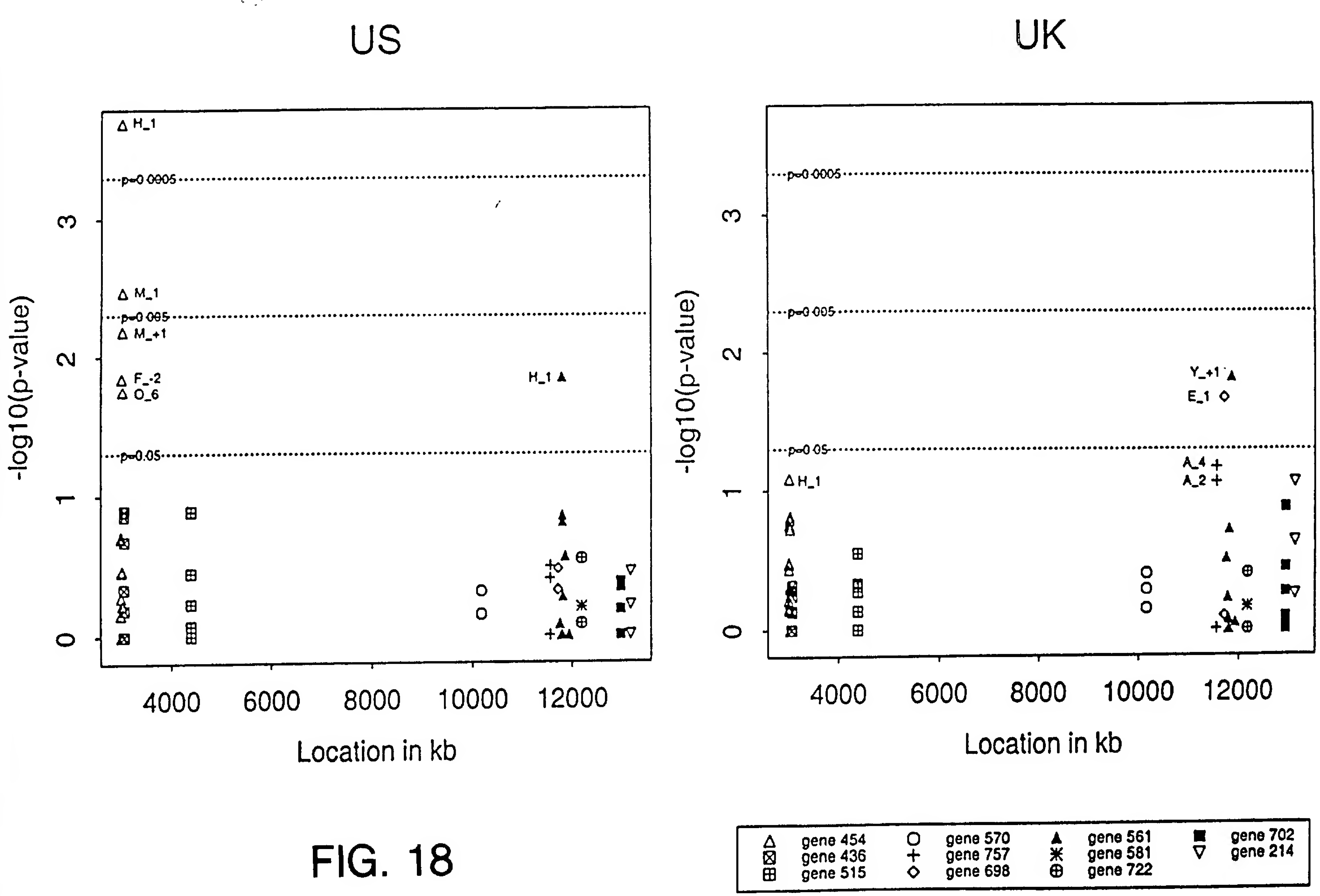


FIG. 18

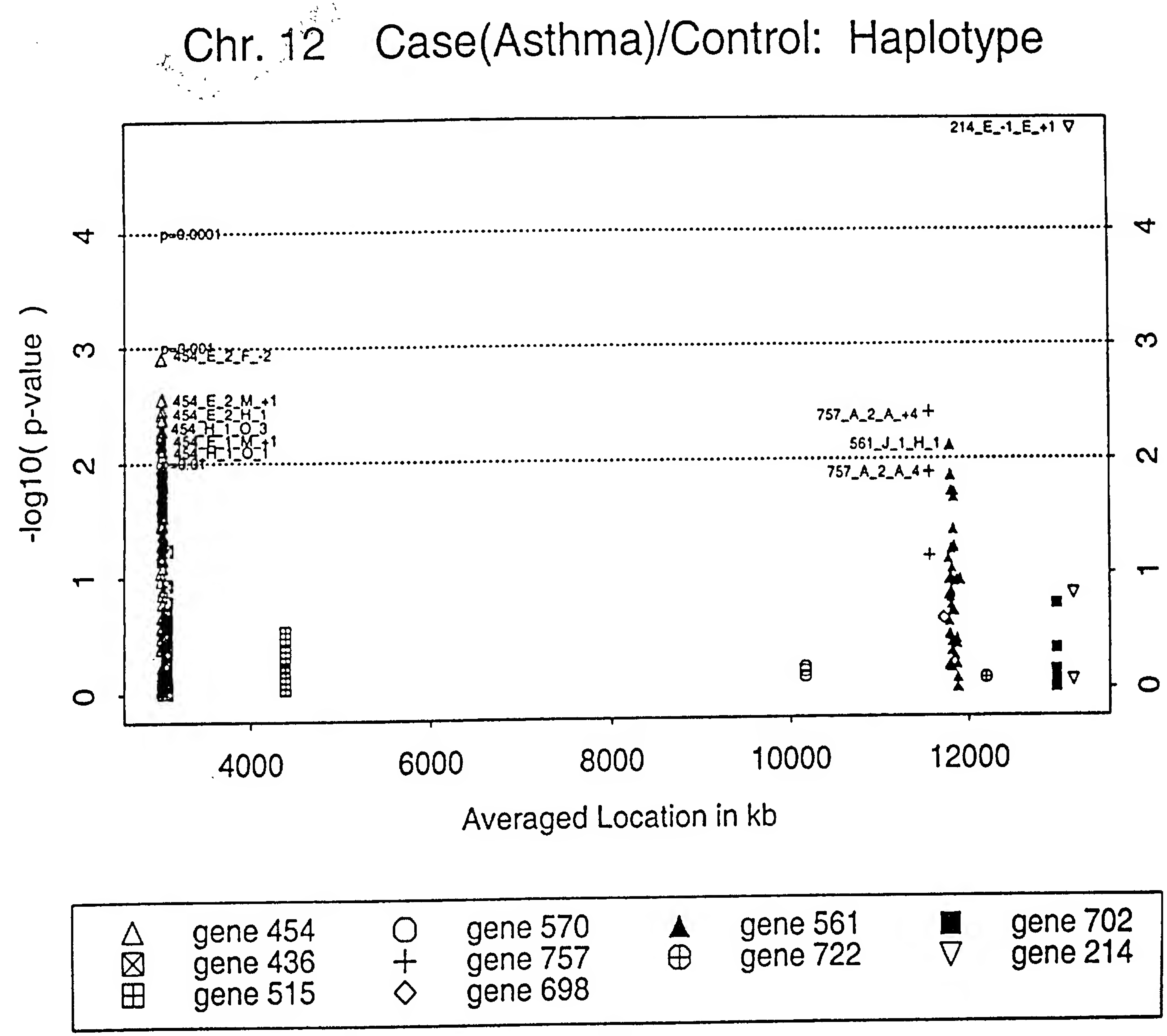
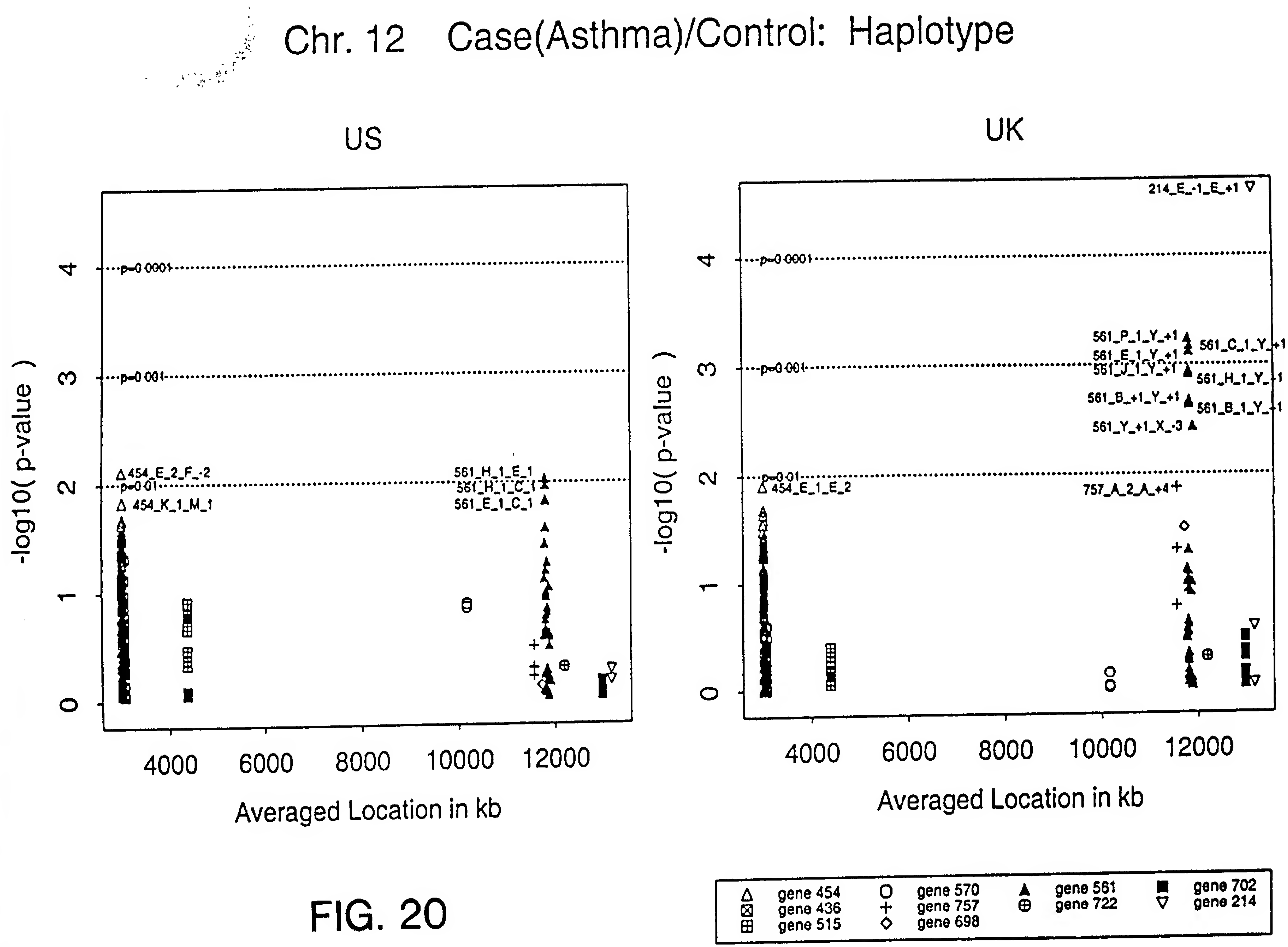

Chr. 12 Case(Asthma)/Control: Haplotype
-log10(p-value)
Averaged Location in kb
p=0.0001
p=0.001
p=0.01
454_E_2_F_-2
454_E_2_M_+1
454_E_2_H_1
454_H_1_O_3
454_E_1_M_+1
454_H_1_O_1
757_A_2_A_+4
561_J_1_H_1
757_A_2_A_4
214_E_-1_E_+1
4000
6000
8000
10000
12000
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 722
gene 702
gene 214

FIG. 19



Chr. 12 Case(Asthma)/Control: Haplotype
US
UK
-log10(p-value)
p=0.0001
p=0.001
p=0.01
454_E_2_F_-2
454_K_1_M_1
561_H_1_E_1
561_H_1_C_1
561_E_1_C_1
214_E_-1_E_+1
561_P_1_Y_+1
561_E_1_Y_+1
561_J_1_Y_+1
561_C_1_Y_+1
561_H_1_Y_-1
561_B_+1_Y_+1
561_B_1_Y_-1
561_Y_+1_X_-3
757_A_2_A_+4
454_E_1_E_2
0
1
2
3
4
4000
6000
8000
10000
12000
Averaged Location in kb
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 722
gene 702
gene 214

FIG. 20

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

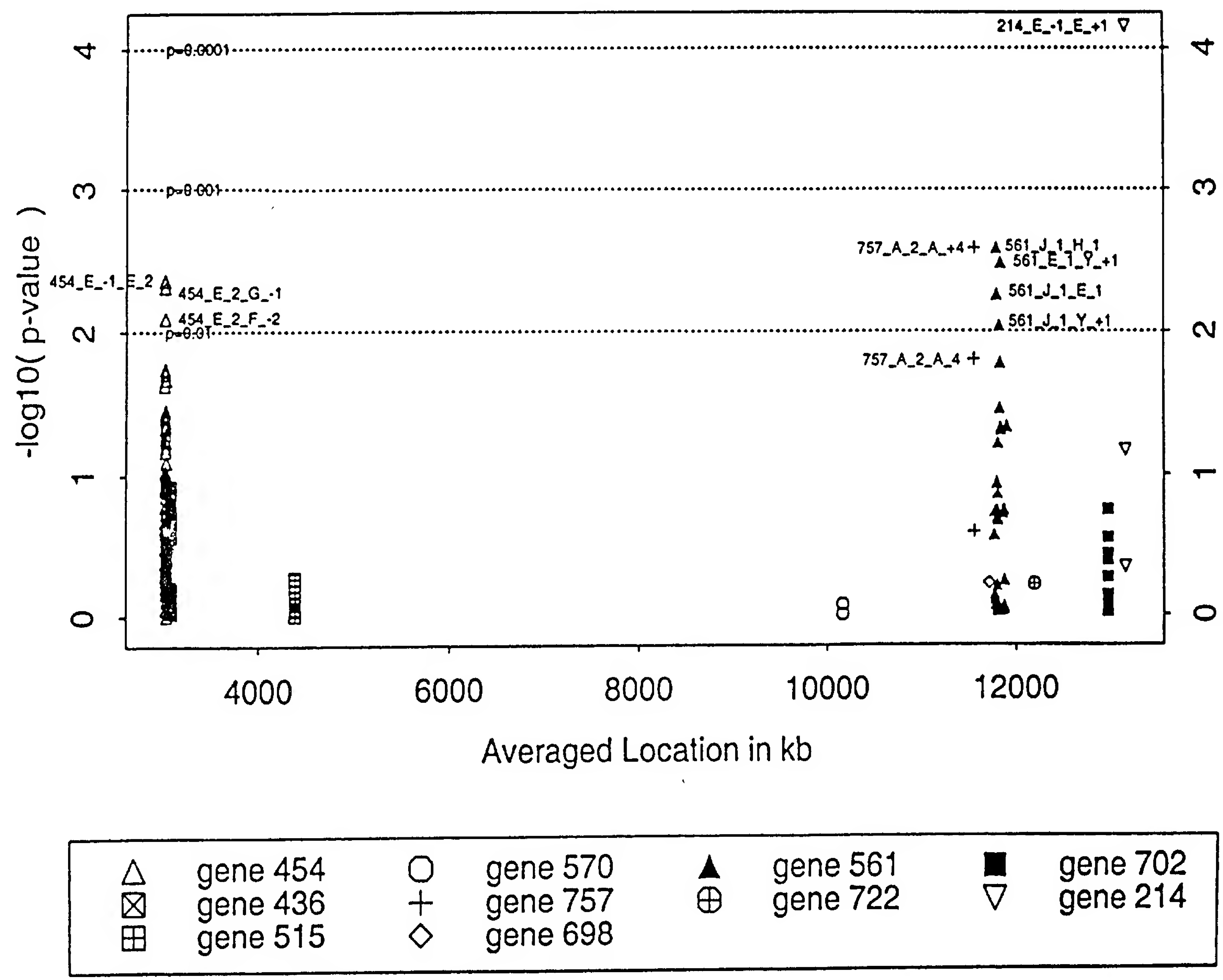


FIG. 21

Chr. 12 Case(BHR (PC20 <= 16 mg/ml) & Asthma)/Control: Haplotype

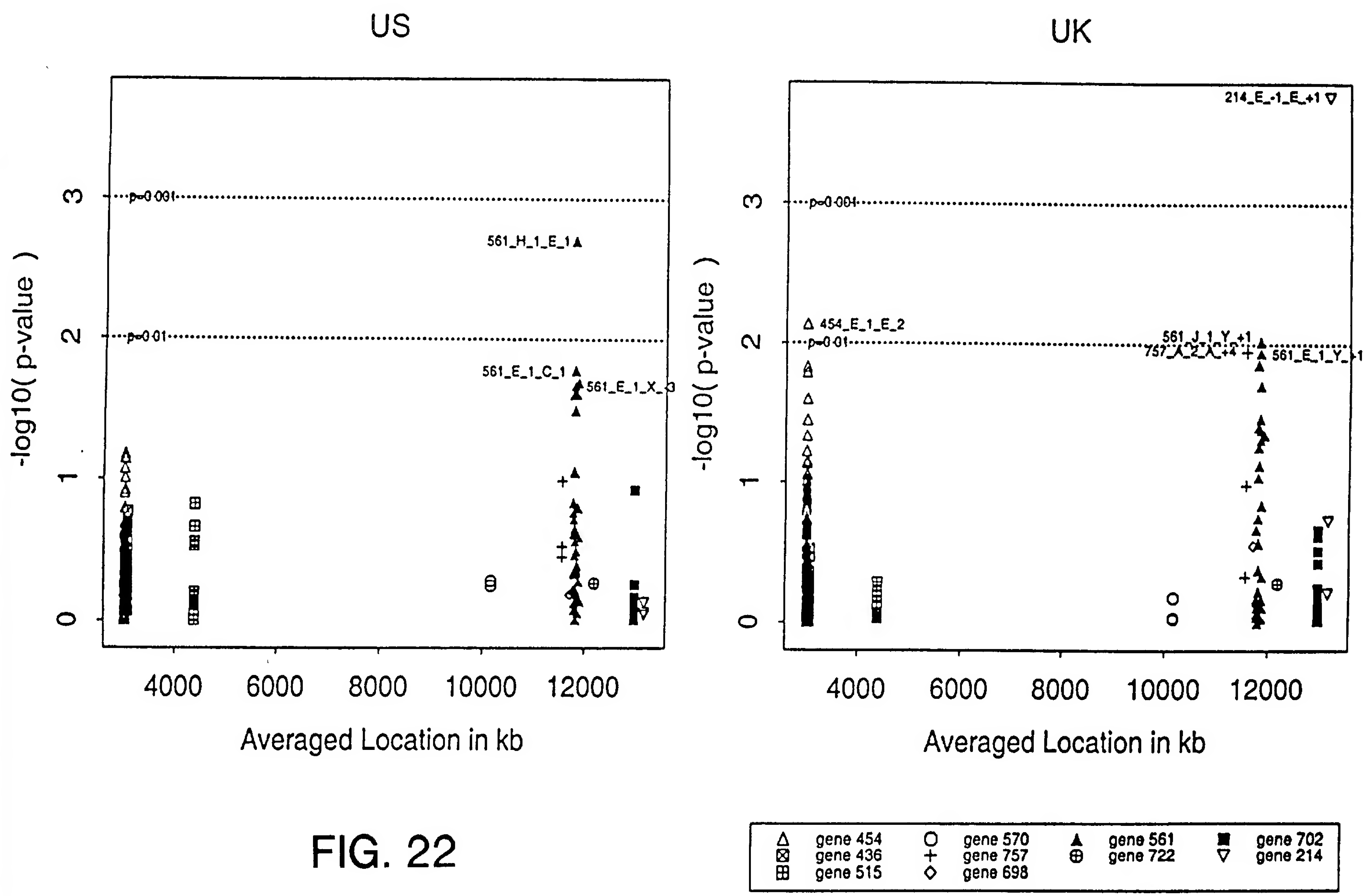


FIG. 22

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

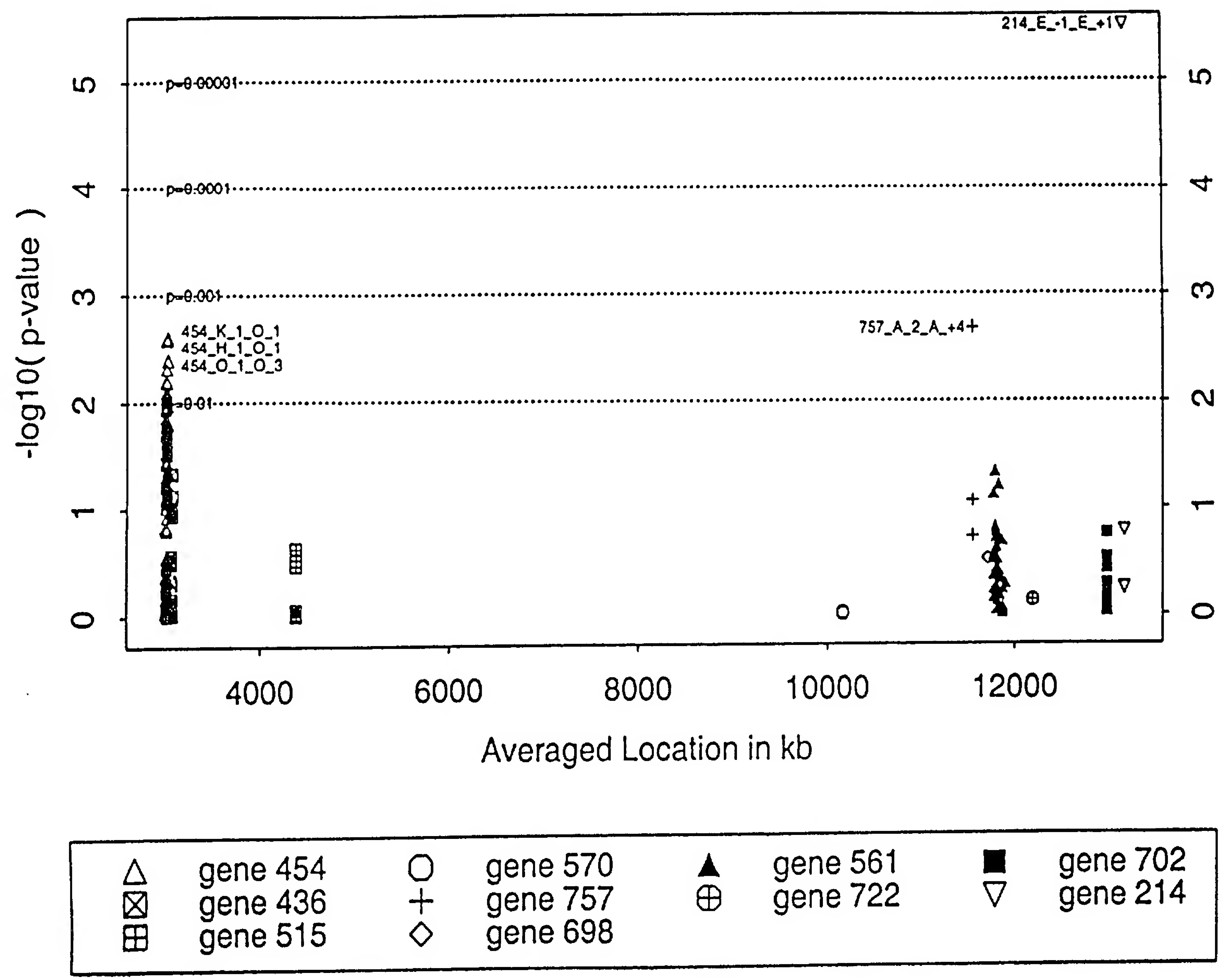


FIG. 23

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

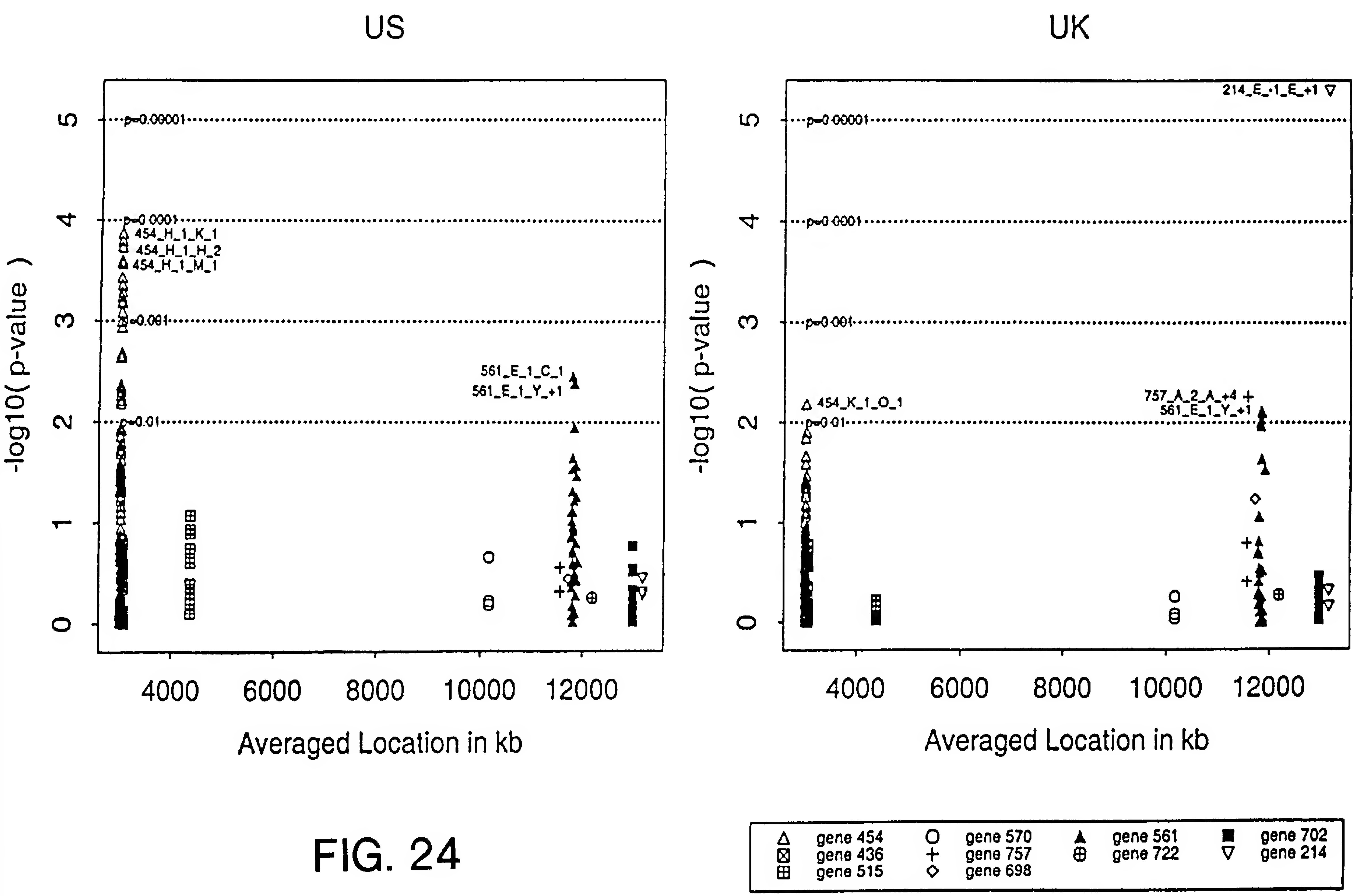


FIG. 24

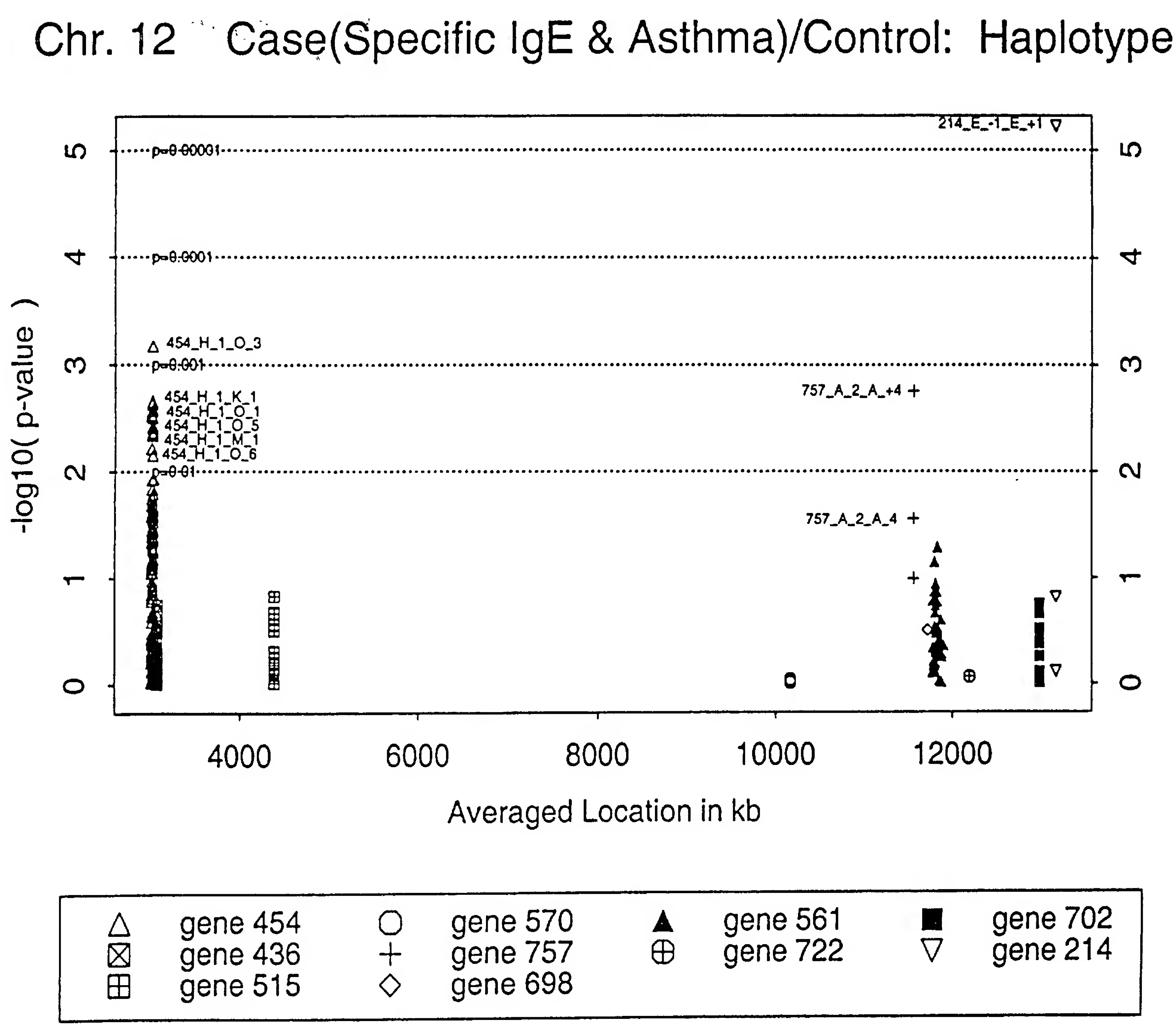
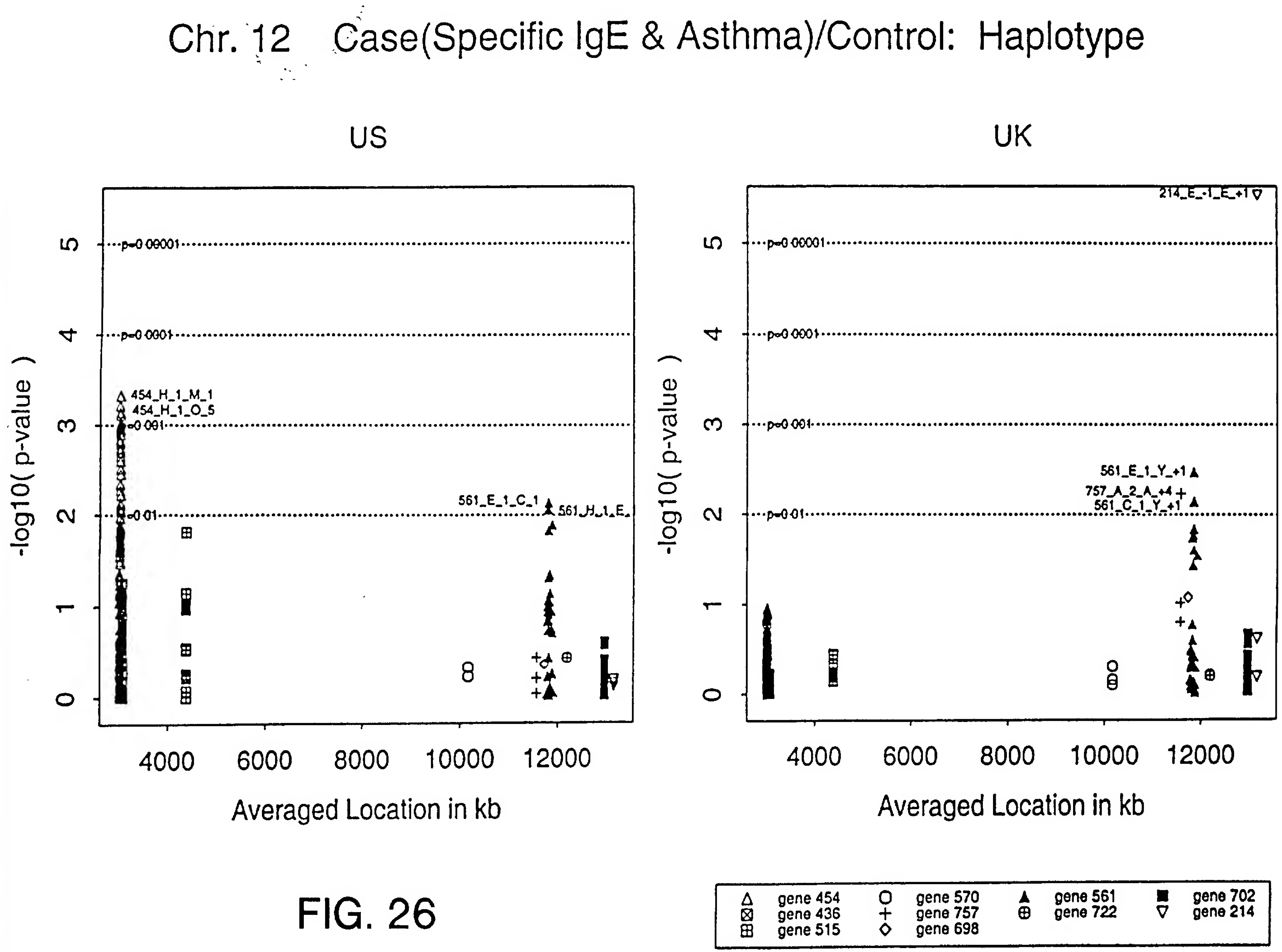

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype
-log10(p-value)
Averaged Location in kb
4000
6000
8000
10000
12000
0
1
2
3
4
5
p=0.00001
p=0.0001
p=0.001
p=0.01
454_H_1_O_3
454_H_1_K_1
454_H_1_O_1
454_H_1_O_5
454_H_1_M_1
454_H_1_O_6
757_A_2_A_+4
757_A_2_A_4
214_E_-1_E_+1
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 722
gene 702
gene 214

FIG. 25



Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype
US
UK
-log10(p-value)
p=0.00001
p=0.0001
p=0.001
p=0.01
454_H_1_M_1
454_H_1_O_5
561_E_1_C_1
561_H_1_E
214_E_-1_E_+1
561_E_1_Y_+1
757_A_2_A_+4
561_C_1_Y_+1
Averaged Location in kb
gene 454
gene 436
gene 515
gene 570
gene 757
gene 698
gene 561
gene 722
gene 702
gene 214

FIG. 26

```
        10                  30                  50
         .         .         .         .         .         .
CTTGGAAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTCGATCAGACC

        70                  90                 110
         .         .         .         .         .         .
CAAGCTTTGGGAGACCGCTGGGGAAATTTCCCACTTCCTCTCCTGAGACCAGGAACTCAG

       130                 150                 170
         .         .         .         .         .         .
CAGAGAAACTTTGTGGAAAATGAACTGAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA

       190                 210                 230
         .         .         .         .         .         .
TCCCATCATGCAGGCCTTCCCACAAGGGCCCGGCAGCATGACAAGGTGAAGGCAGAGTAT

       250                 270                 290
         .         .         .         .         .         .
GTGCATCTCAACCAYCCGCTCACCCTCGTGACCAGAGAGCGCGATTTGGCCGTGAAGGAG

       310                 330                 350
         .         .         .         .         .         .
AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCCTGAAGCATATGCGAGAG
                                                   MetArgGlu

       370                 390                 410
         .         .         .         .         .         .
GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT
AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer

       430                 450                 470
         .         .         .         .         .         .
GCCAAGCAGCAGGAAATTGACCTTCTGCAGAAGTCCAAGGTTCGAGAGCTGGAAGAGAAA
AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluGluLys

       490                 510                 530
         .         .         .         .         .         .
TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG
CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln

       550                 570                 590
         .         .         .         .         .         .
CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCCTGGACATCTCCACG
HisAlaGlyLysIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr
```

FIG. 27A

610 630 650

GCCCCCAGCAAGCCTTTCCCACAGTTCATGAATGGCCTAGCCACCTCCCTCGGCAAAGGT
AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly

670 690 710

CAGGAGAGCGCTATTGGAGGCAGCTCTGCGATCGGTGAATATATCCGGCCCCTTCCGCAG
GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln

730 750 770

CCTGGTGACAGGCCGGAGCCTCTGTCCGCCAAGCCCACCTTCCTGTCGAGATCCGGTAGC
ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer

790 810 830

GCAAGATGCAGATCTGAGTCAGACATGGAGAATGAACGGAATTCCAATACCTCCAAGCAG
AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln

850 870 890

AGATACTCGGGGAAGGTCCACCTCTGTGTTGCCCGCTATAGTTACAACCCCTTCGATGGA
ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly

910 930 950

CCGAACGAGAACCCCGAAGCTGAGCTGCCCCTCACGGCGGGAAAATACCTCTACGTCTAT
ProAsnGluAsnProGluAlaGluLeuProLeuThrAlaGlyLysTyrLeuTyrValTyr

970 990 1010

GGAGACATGGATGAGGATGGGTTCTATGAAGGAGAGCTCCTCGATGGCCAGAGGGGTCTG
GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu

1030 1050 1070

GTGCCCTCCAACTTCGTGGACTTTGTGCAGGACAACGAGTCGCGGTTGGCAAGCACGCTG
ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu

1090 1110 1130

GGGAACGAGCAGGATCAGAACTTCATCAACCATTCCGGCATCGGCCTGGAGGGAGAGCAC
GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis

1150 1170 1190

ATCCTGGACCTCCACTCCCCAACCCACATAGATGCGGGCATCACCGACAACAGTGCCGGG

FIG. 27B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

```
        1210                1230                1250
ACCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

        1270                1290                1310
ACCCTCATCAAACAACTCGCCAAAAGTGTTATTGTGGGCTGGGAGCCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

        1330                1350                1370
CCAGGATGGGGAACGGTGAGCAGCTACAACGTCCTGGTGGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

        1390                1410                1430
CTCACGCTGGGGAGCAGAACTAAAGCCCTCATCGAGAAGCTCAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

        1450                1470                1490
TACCGCATCTCCGTGCAGTGCGTCACCAGCAGGGGCAGCTCGGATGAGCTGCAGTGCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

        1510                1530                1550
CTGCTGGTGGGCAAGGACGTGGTGGTGGCCCCCTCCCACCTGCGGGTGGACAACATCACG
LeuLeuValGlyLysAspValValValAlaProSerHisLeuArgValAspAsnIleThr

        1570                1590                1610
CAGATCTCCGCCCAGCTCTCCTGGCTACCCACCAACAGCAACTACAGCCACGTCATCTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

        1630                1650                1670
CTCAACGAGGAGGAGTTCGACATCGTCAAGGCCGCCAGGTACAAGTACCAGTTCTTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

        1690                1710                1730
CTCAGGCCCAACATGGCCTATAAGGTGAAGGTTCTGGCCAAACCCCACCAGATGCCGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp
```

FIG. 27C

1750 1770 1790

CAGCTCCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTTGTGGAGTTCTCCACGTTGCCT
GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810 1830 1850

GCAGGACCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC
AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870 1890 1910

ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCCACCGGGCTGTCCAATGGCGCAAAC
IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930 1950 1970

GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTTCCCCACG
ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990 2010 2030

GCAGACAGCACGGCCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC
AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050 2070 2090

GTGCGGACCCTCTCCGCCCAGGGCGAGTCCGTGGACTCTGCAGTTGCTGCCGTTCCCCCC
ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110 2130 2150

GAGCTCCTGGTGCCTCCTACCCCCCACCCGAGACCTGCACCCCAATCAAAGCCATTAGCA
GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170 2190 2210

AGTTCTGGAGTCCCCGAAACCAAAGACGAGCACCTGGGTCCCCACGCCAGGATGGATGAG
SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230 2250 2270

GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGCCGCCCGTG
AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290 2310 2330

GGCCCCGGAAGGCGGTCGCCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCG

FIG. 27D

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350 2370 2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410 2430 2450

AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470 2490 2510

TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530 2550 2570

GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590 2610 2630

CACACAGAGAGCAGCCGGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGluGlu

2650 2670 2690

CTGTATTCTGAAATGCAGCTGGAAGATGGGGGAAGGAGGCGGCCCAGCGGCACGTCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgArgProSerGlyThrSerHis

2710 2730 2750

AATGCCCTCAAGATTTTAGGGAACCCAGCCTCTGCAGGACGGGTGGATCACATGGGCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770 2790 2810

AGGTTTCCCCGTGGCAGCGCTGGTCCTCAGAGGTCCCGGCCCGTGACAGTCCCATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830 2850 2870

GACGATTACGGGCGAGACCGCCTTTCTCCAGACTTCTATGAAGAGTCAGAAACTGACCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

FIG. 27E

2890 2910 2930

GGTGCCGAAGAGCTCCCGGCCCGGATCTTTGTGGCTCTCTTTGACTACGACCCGCTCACC
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr

2950 2970 2990

ATGTCCCCAAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTTAAAGAAGGCCAGATCATC
MetSerProAsnProAspAlaAlaGluGluGluLeuProPheLysGluGlyGlnIleIle

3010 3030 3050

AAGGTTTATGGTGATAAAGACGCTGATGGATTCTACCGTGGGGAAACCTGTGCCCGGCTT
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu

3070 3090 3110

GGCCTTATTCCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp

3130 3150 3170

CAGCTTCTTAGACAGGGCTTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAGC
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer

3190 3210 3230

AGGAGAAGTGGCAGGCGTCATTCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr

3250 3270 3290

GACCCCAGAGAAAGCTCGCCCAACGTCGATGTCGAGGCCGAACTTACATTTTGCACAGGA
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly

3310 3330 3350

GATATTATTACAGTTTTTGGTGAAATTGATGAAGATGGATTTTATTATGGGGAGCTGAAC
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn

3370 3390 3410

GGGCAGAAAGGCCTTGTGCCCTCAAACTTCTTGGAAGAAGTGCCTGATGACGTAGAAGTC
GlyGlnLysGlyLeuValProSerAsnPheLeuGluGluValProAspAspValGluVal

3430 3450 3470

TATCTTTCTGATGCTCCATCCCACTACTCTCAAGATACGCCAATGCGCTCAAAGGCAAAA

FIG. 27F

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490 3510 3530

AGGAAGAAGAGTGTTCATTTCATACCTTAATCAGGCAATGTAGCCTTCACGTAAGTGAGC
ArgLysLysSerValHisPheIleProEnd

3550 3570 3590

AACTGAAGATACCGATAAAGATACCAACTTAAGCTACCTTAACCGGGCCAGTGTGGTAGA

3610 3630 3650

CTTAAGGCTTCATTGTGGGGTTAAAAAAAAAAAAAGATACAAAGAAATATGTCTCAAAAA

3670 3690 3710

ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAAGCAACTGAATTTA

3730 3750 3770

TAGTGAAGCAAATCATCTTTAATAATCATTTCCTACTATTTGCATTAAGAATATTTGAAA

3790 3810 3830

GGCCAACATTGGGAACATATTTCTTAACAAGCTAACTGTGTGTTTACATAGAGAGAGCTG

3850 3870 3890

CATATTGCATTGTTAGCCACTCTTGGAAAAAGCACAACCTAACAAACATGTTTACTATAG

3910 3930 3950

GAAGCTTTACTTTAGAAACTTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970 3990 4010

CGAGTGTTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTTTCCTTA

4030 4050 4070

AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCCTCAAAGCACAATCATCCTG

4090 4110 4130

TGACAGAAGTTGCTGCAACACGCGTTTGTTGTTGGTATACCAATGCAATACTAAGTTGAT

FIG. 27G

4150 4170 4190

GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTTCAGGTGTACTTT

4210 4230 4250

GGGATGCTTTACTAGGTGTTTTCCATTAGAATTAGACCTTGATTTTAAATCCAAGCAAGC

4270 4290 4310

TTGAAGCCCCTTGGCTTACAGCATTTGCCTGCTGAATACTAAACACTCACATGGCAAGAG

4330 4350 4370

TTGCTCTGGAGAGGTAGGGCCAGAGGAATGCTGCTGCACTGCCAACTCAGGCACATGCTT

4390 4410 4430

AGCTGTAAAGGGAAGCGAGGTGAAGTCGTCCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4450 4470 4490

TCTGAAGCACTATTAAGCGCTTAACGTATATTTAAATACTACCATGTGCTATCTACTGAG

4510 4530 4550

GAAGATTCATGTTCAATTATTTGGAAATAATGCAAGCATCCACTAAGGGCCTTTAAGCTT

4570 4590 4610

TCTTTGATTATAATTAAGGTTCATTTTAGTTTTTTTTTTTTCTTTCAACCAGTGTGCCAT

4630 4650 4670

CTCCAATATTTCTATAGTATACCAACCACCCCAGGAATGCACTTTAACAATATCAGGATT

4690 4710 4730

TTATATAACCAAATAGTTTCAAATACAACAAAATTCCCTTTATGAACTTTCGCTTTTTAA

4750 4770 4790

GACTACTGATGGGTACTCGGCCAACTTTACTATCAACCTAATTTCAGATCATGTCTCCCC

FIG. 27H

4810 4830 4850

TGCCCTTAGTCTTCATTTATGAAGTGAATTATTACCTGCCTTAGCTTTGCCAAAGCAACG

4870 4890 4910

GCCACCCCGCACTCCCTCGAGACAGAGAAACGGAACCCACACATTTATGTCTGGGGCCTC

4930 4950 4970

TCTCTGGCGTGCTGTGGGAGAGGACCTTTGCTTCTCATGGCATACTTCAACAACTGAAAG

4990 5010 5030

AACAAATGAACCCCCCTGACCTTTCCTGGTGGGAAACGGGGACAGTACGATGTTACCAAG

5050 5070 5090

TGAATTCTGTTGTTGGCGCTCACACACTCAATAAACTGTAACACTGTACCTACTAGGTTC

5110 5130 5150

CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCCACAGTCCATCTCCATTCGG

5170 5190 5210

GGTCACCTACGTCATCTATGGGTTCTGGTAGTCCTGGGAGAGGCAGGGAAATGTCCTCGA

5230 5250 5270

AAAAGAAAAAGGGGCTGCTTTCCAAAGGCAAGAAACTGCTGAAAAAGCTGGGTGCAGTGA

5290 5310 5330

AATGATTCATGTGCTTCCGGACAACTGCCAAATCTATGTAATTTTCTTTAATTCCAAACT

5350 5370 5390

AGGGCTTTCATGACTCAAGTACTTCCTAAAAAAACCCAATCTTCTCCCCTGACACCAGTA

5410 5430 5450

GAGAAATGCACTTTTGCACTACCAACCACTTTAAACCAACCACGAGAACAAAGAGGAGCG

5470 5490 5510

FIG. 27I

GTTGCTCTCTGTCACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTTGGGAGGTG

5530 5550 5570

GGAGGGGACGTCTTATTAACAAACGGGGGCGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590 5610 5630

CCTGTAATTCCAGTCTTTGTGCATTTGTCATCTGCCCTTAAAGGAATGATTTTCAACCTT

5650 5670 5690

TCTCCCTTCTCAAAATGCTTGCCTCATAATGCATAACTTTCACTTTGACTCTGGTCTTGA

5710 5730 5750

AATTCCTAGTTTAATTCGCCTTGATGTTCTGCCTTATAAATGCACAATGATTTGTACTGT

5770 5790 5810

CTAATAAAAACAGTGTATACTTTGTATGTGTCGTGCATTCAGTGGTCTTCATCCTGACAC

5830 5850 5870

AGTGGTTCGAGATCAAGTTGTACAGGCTGTGCATTTTAAGATACTAGTTTCAGTCTTTCA

5890 5910 5930

AAGCCAGCCAGGCTACACACAGAAAATGTTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950 5970 5990

AGAAAGTAACTTTGTTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010 6030 6050

TCATTGCTTTTAATGTTCTATTCTGTGGCATATGGTTTTCTGTTACTTTCGTTGTCAAAA

6070 6090 6110

TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130 6150 6170

ACACCAAAACCAGACTCAATTTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

FIG. 27J

```
     6190                6210                6230
        .         .         .         .         .         .
TGGCATTTGAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC

     6250                6270                6290
        .         .         .         .         .         .
TTTTGTAATTCTTGTCCACTTGTAAATTGTTTTTACTCTTTATACATACTTTTCAGACTG

     6310                6330                6350
        .         .         .         .         .         .
CCTTTCTTTTGTAATTTATGGACGGTTTATAAATGAATGACAAAGCTTTCCCCATTGTGT

     6370                6390                6410
        .         .         .         .         .         .
CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTTATTATTAAAGG

     6430                6450                6470
        .         .         .         .         .         .
AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGTGCATGTGCACAGTTAGTGTAAAATA

     6490
        .         .
TTTTCTAGAAATAAAATTTGTTATTTTAT
```

FIG. 27K

```
        10                  30                  50
         .         .         .         .         .         .
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAAGCCTGTGCACCTGGCCCTGTGC
               MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys

        70                  90                 110
         .         .         .         .         .         .
ATGGGCACATGCTGGAGCCGCCCGTGGGCCCCGCATCCTGCCACAGCCACAGGGCACCCC
MetGlyThrCysTrpSerArgProTrpAlaProHisProAlaThrAlaThrGlyHisPro

       130                 150                 170
         .         .         .         .         .         .
GGTGTCCACCACCGTCGCCAAGGCCATGGCCCGGGAGGCCGCGCAGAGGGTGGCGAGAGC
GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer

       190                 210                 230
         .         .         .         .         .         .
AGCAGGTTAGAGAAAAGGAGCGTCTTCCTAGAGAGAAGCAGCGCGGGGCAGTACGCCGCC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

       250                 270                 290
         .         .         .         .         .         .
TCAGACGAGGAGGACGCCTATGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

       310                 330                 350
         .         .         .         .         .         .
GACTTCCTGAAAGGCTCTGAACTTGGCAAGCAGGGAAACTGAGGCCCACAGAATTGAGAA
AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd

       370                 390                 410
         .         .         .         .         .         .
TTTTTGTCCATGATTACGCAGATGGTCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG

       430                 450                 470
         .         .         .         .         .         .
CCTGAAGAAGACCTGTTTCCACGCCTTTCCCCATGTGCCACGTTCTCCTCACCTATCCAG

       490                 510                 530
         .         .         .         .         .         .
GAGTGAATCATCACCTTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA

       550                 570                 590
         .         .         .         .         .         .
GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTTGAGATCGGCATTCAGC
```

FIG. 28A

610 630 650

GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCCACCTG

670 690 710

GGGCTGAGTGTGACTGAGGCCCTGAATTTTTACTTCTATAAAATTAGTTCCAGATTAGTT

730 750 770

TACATTCCTAATTAGTTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA

790 810 830

CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTTCTAGAGAAGAGTAGAA

850 870 890

ACACAGCGGCAGAAACACAGCTCTGCACTTCCGAGGGCCTCCCACTCCTTCTGATGAGAC

910 930 950

TGCAGAGGAAGTCTGTTTGGCCAAGCATGCTATTAACACGTTTTCCTGCTTGTTTTGTTT

970 990 1010

TTTAACAGAGCAAACAGGTCTGTTTCTATTAAAATTTAAAAAGCGTTAATATTTARCAGC

1030 1050 1070

ATTGTTTTATGTTGTATTCATAACATAATAATATAACAATATATTAATTGTTAATATATA

1090 1110 1130

TTGTTAATAATATAATAATATAACATAAAATAAGTGATACTTATTTTCCATTTACAGTTG

1150 1170 1190

AGATATTTTCTTTAAAAGTAACGTTAAATATTGATTCAATTCAAAGAATACATTCATTAA

1210 1230 1250

TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT

1270 1290 1310

FIG. 28B

TGAGCTGGTGCACAGACTGCCAGTTTTACAACCCGGGAAGTGTTCCCTGACCATCCGCTT

1330 1350 1370

CCCCATGCTGCCCGCCCCGTCACATGAGCCCTTACCCCCTGGCGCTATCCCATCTGCTCC

1390 1410 1430

AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTTAGTTGACTACGGTATCTCTAG

1450 1470 1490

CATTTCACACATAGTAGGTGCTCAATGAATGTTTGTCGAATGAATGAATGAAAGAAGGGA

1510 1530 1550

GGCTGAGAGTAGCTGGGACATTTGCTCTGAAAAAATCACCTCCATTCTCCCAATATTACA

1570 1590 1610

AAAGCATTTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAAATAATATCTTT

1630 1650

AGTTATCTATTTTTAAAAGTAAAAAAAAACCTCGTGCCGAAGTC

FIG. 28C